

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 11:23:43 ; Search time 3628.41 Seconds
(without alignments)
78.116 Million cell updates/sec

Title: US-09-913-325-4
Perfect score: 21
Sequence: 1 cagcagcagagcttcacatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	100.0	85	9	AM276802	AM276802 xp66a01.x
2	100.0	100	9	BF920141	BF920141 MR1-NT017
3	100.0	102	10	BF958934	BF958934 PM1-NN120
4	100.0	119	9	AM901233	AM901233 CM4-NN101
5	100.0	142	10	DA5267	DA5267 HOMHG1194 H
6	100.0	148	10	BF846357	BF846357 PM1-EN006
7	100.0	149	10	R47195	R47195 CBS-389 Sub
8	100.0	169	10	BE766895	BE766895 RC2-NT011
9	100.0	177	9	AL048592	AL048592 DKEZ5864
10	100.0	183	10	BI032792	BI032792 MR4-NN018
11	100.0	184	10	BF958930	BF958930 PM1-NN120
12	100.0	185	10	BI036860	BI036860 MR4-NT014
13	100.0	196	9	A1745406	A1745406 wC37d01.x
14	100.0	197	10	BI036862	BI036862 MR4-NT014
15	100.0	201	10	BF957666	BF957666 PM1-NN120
16	100.0	203	10	BF957653	BF957653 PM1-NN120
17	100.0	207	10	BF957858	BF957858 PM1-NN120

Result No.	Score	Query Match	Length DB	ID	Description
18	100.0	224	9	AM161224	AM161224 au70a10.y
19	100.0	226	10	BF935119	BF935119 MR4-NT014
20	100.0	236	10	BF948789	BF948789 MR3-NN021
21	100.0	238	10	BF923639	BF923639 MR4-NT014
22	100.0	239	10	BG889974	BG889974 HOA21-1-C
23	100.0	243	9	AA336628	AA336628 EST41242
24	100.0	244	10	BE766870	BE766870 RC2-NT011
25	100.0	248	10	BF923643	BF923643 MR4-NT014
26	100.0	249	10	BF945175	BF945175 PM1-NN120
27	100.0	252	10	BF923633	BF923633 MR4-NT014
28	100.0	252	10	BF963107	BF963107 PM1-NN120
29	100.0	253	10	BF887875	BF887875 QV2-NT017
30	100.0	253	10	BI041998	BI041998 MR4-NT014
31	100.0	256	10	BI041248	BI041248 MR4-NT014
32	100.0	258	10	BF961150	BF961150 PM1-NN120
33	100.0	262	10	BF947155	BF947155 MR3-NN021
34	100.0	263	10	BE899032	BE899032 601682590
35	100.0	265	10	BF961152	BF961152 PM1-NN120
36	100.0	268	10	BF920149	BF920149 MR1-NT017
37	100.0	269	10	BF948799	BF948799 MR3-NN021
38	100.0	272	10	BF956582	BF956582 PM1-NN120
39	100.0	273	10	BF947794	BF947794 MR3-NN021
40	100.0	273	10	BF956584	BF956584 PM1-NN120
41	100.0	274	10	BI036852	BI036852 MR4-NT014
42	100.0	283	10	BF947214	BF947214 MR3-NN021
43	100.0	287	10	BI041483	BI041483 MR4-NT014
44	100.0	293	9	AA318247	AA318247 EST20305
45	100.0	297	10	BF949666	BF949666 QV2-NN119

ALIGNMENTS

RESULT 1
AM276802/c
LOCUS
DEFINITION
xp66a01.x1 NCI-CGAP_Ov39 Homo sapiens CDNA clone IMAGE:2745288 3'
similar to gb:x14723 CLUSTERIN PRECURSOR (HUMAN); mRNA sequence.
AM276802
AM276802.1 GI:6663832
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 85)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www.bio.llnl.gov/btrp/image/image.html

FEATURES
source
1. 85
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2745288"
/clone_lib="NCI-CGAP_Ov39"
/sex="female"
/tissue_type="papillary serous ovarian metastasis"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pAMP10; CDNA made by oligo-dT
Possible reversed clone: polyt not found
Seq primer: -40up from Gibco.
Location/Qualifiers

priming. Non-directionally cloned into the UDG sites of
 PAMP10. Size-selected on agarose gel, average insert
 size 500 bp. Primary library: non-amplified. cDNA
 Library Preparation: David B. Kitzman, Ph.D (NCI).
 Reference: Kitzman et al. (1996) Cancer Research
 56:5380-5383."

BASE COUNT 18 a 21 c 30 g 16 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 85;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagctctcatcat 21
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 Db 82 CAGCAGCAGAGCTCTCATCAT 62

RESULT 2
 BF920141 100 bp mRNA linear EST 19-JAN-2001
 LOCUS MRI-NT0179-071100-003-f02 NT0179 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF920141
 VERSION BF920141.1 GI:12316029
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 102)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MR1-NT0179-
 071100-003-f02&t3=2000-11-07&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 11
 High quality sequence stop: 100.
 Location/Qualifiers

FEATURES
 source
 1..100
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NT0179"
 /dev_stage="Adult"

/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 21 a 34 c 20 g 25 t
 ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 100;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagctctcatcat 21
 ||||||||||||||||||||
 Db 56 CAGCAGCAGAGCTCTCATCAT 76

RESULT 3
 BF958934 102 bp mRNA linear EST 22-JAN-2001
 LOCUS PML-NN1200-011200-009-b07 NN1200 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF958934
 VERSION BF958934.1 GI:12376209
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 102)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PML&t2=PML-NN1200-
 011200-009-b07&t3=2000-12-01&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 11
 High quality sequence stop: 101.
 Location/Qualifiers

FEATURES
 source
 1..102
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NN1200"
 /dev_stage="Adult"

/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 21 a 25 c 38 g 18 t
 ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 102;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagctctcatcat 21
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 Db 91 CAGCAGCAGAGCTCTCATCAT 71

RESULT 4

AW901233/c
LOCUS AW901233 119 bp mRNA linear EST 24-MAY-2000
DEFINITION CM4-NN1011-100300-110-g04 NN1011 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW901233
VERSION AW901233.1 GI:8065542
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 119)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL Contact: Simpson A.J.G.
MEDLINE Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4-NN1011-100
300-110-g04&t3=2000-03-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 118.
Location/Qualifiers
1..119
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1011"
/dev_stage="Adult"
/note="Organ: nervous, normal. Vector: puc18; Site_1: Smat;
Site_2: Smat; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 21 a 28 c 46 g 23 t 1 others
ORIGIN
Query Match 100.0%; Score 21; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cagcagcagagcttcacat 21
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Db 103 CAGCAGCAGAGCTTCATCAT 83
RESULT 5
LOCUS D45267 142 bp mRNA linear EST 30-DEC-1995
DEFINITION HMMHC1194 Human cerebral cortex Homo sapiens cDNA, mRNA sequence.
ACCESSION D45267
VERSION D45267.1 GI:1136645
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 142)
AUTHORS Takahashi, N., Hashida, H., Zhao, N., Misumi, Y. and Sakaki, Y.
TITLE High-density cDNA filter analysis of the expression profiles of the
genes preferentially expressed in human brain
JOURNAL Gene 164, 219-227 (1995)
MEDLINE 96069586
COMMENT Contact: Nobuaki Takahashi
Institute of Medical Science
University of Tokyo
Shirokanedai 4-6-1, Minato-ku, Tokyo, Japan 108
Tel: 03-5449-5625
Fax: 03-5449-5445.
Location/Qualifiers
1..142
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human cerebral cortex"
/note="Adult male cerebral cortex tissue."
BASE COUNT 26 a 31 c 55 g 30 t
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 142;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cagcagcagagcttcacat 21
|||||
Db 79 CAGCAGCAGAGCTTCATCAT 59
RESULT 6
LOCUS BF846357 148 bp mRNA linear EST 16-JAN-2001
DEFINITION PM1-EN0065-231000-002-b01 EN0065 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF846357
VERSION BF846357.1 GI:12233611
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 148)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL Contact: Simpson A.J.G.
MEDLINE Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1-EN0065-
231000-002-b01&t3=2000-10-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 110.
Location/Qualifiers
1..148
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="EN0065"
/dev_stage="Adult"

/note="Organ: lung_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 24 a 56 c 41 g 27 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcagcagagcttcacatcat 21
|||||
Db 34 CAGCAGCAGAGCTTCATCAT 54

RESULT 7
R47195 149 bp mRNA linear EST 12-DEC-1995
LOCUS R47195
DEFINITION CBS-389 Subtractive cDNA library ocular ciliary body Homo sapiens
CDNA clone CBS-389 5' end similar to TRPM-2 (clusterin) (accession number M64722), mRNA sequence.
R47195
VERSION R47195.1 GI:807537
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 149)
AUTHORS Escribano, J., Ortego, J. and Coca-Prados, M.
TITLE Isolation and characterization of cell-specific cDNA clones from a subtractive library of the ocular ciliary body of a single normal human donor: Transcription and synthesis of plasma proteins

JOURNAL J. Biochem. (Tokyo) 118 (5), 921-931 (1995)
MEDLINE 96318503
COMMENT Contact: Coca-Prados, M.
Department of Ophthalmology and Visual Science
Yale University Medical School
330 Cedar Street, New Haven, CT 06520-8061
Tel: 203/7852742
Fax: 203/7856123
Email: miguel.coca-prados@quickmail.yale.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..149
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBS-389"
/note="Vector: pBluescript II SK; Site_1: EcoRI; Site_2: XhoI; A subtractive cDNA library was developed by hybridizing antisense, single-stranded phagemid DNA (ssDNA) (as pBluescript SK-) from the ocular ciliary body cDNA library (target) of a 34-year-old female donor in lambda-uni-zap XR with biotinylated sense RNA of an ocular cell line cDNA library (driver) in the same vector."

BASE COUNT 33 a 31 c 56 g 29 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 149;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcagcagagcttcacatcat 21
|||||
Db 71 CAGCAGCAGAGCTTCATCAT 51

RESULT 8
BE766895 169 bp mRNA linear EST 19-MAR-2000
LOCUS BE766895/c
DEFINITION RC2-NT0110-050600-013-f03 NT0110 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE766895
VERSION BE766895.1 GI:10196819
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 169)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Mitsuuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=62-RC2-NT0110-050600-013-f03&tl3=2000-06-05&tl4=1)

Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 169.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="lib="NT0110"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 37 a 36 c 59 g 37 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 169;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcagcagagcttcacatcat 21
|||||
Db 59 CAGCAGCAGAGCTTCATCAT 39

RESULT 9
AL048592 177 bp mRNA linear EST 01-MAR-2000
LOCUS AL048592/c
DEFINITION DKFZP586H092_r1 586 (synonym: hutel) Homo sapiens cDNA clone
ACCESSION AL048592
VERSION AL048592.1 GI:4729143
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 177)
AUTHORS Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Poustka, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Poustka A.J.
Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inmestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mping-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp586H092) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1. 177
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DKFZp586H092"
/clone_1lb="586 (synonym: hute1)"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
BASE COUNT 40 a 41 c 64 g 32 t
ORIGIN
Query Match 100.0%; Score 21; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cagcagcagagcttcacat 21
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Db 77 CACCACGACAGCTTCATCAT 57
RESULT 10
BI032792 183 bp mRNA linear EST 14-JUN-2001
LOCUS BI032792
DEFINITION M4-NN0188-220101-204-e01 NN0188 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI032792
VERSION BI032792.1 GI:14439418
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 183)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR4&t2=MR4-NN0188-
220101-204-e01&t3=2001-01-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 183.
FEATURES
source
1. 183
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="NN0188"
/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 28 a 72 c 48 g 35 t
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cagcagcagagcttcacat 21
|||||
Db 69 CAGCAGCAGAGCTTCATCAT 89
RESULT 11
BF958930 184 bp mRNA linear EST 22-JAN-2001
LOCUS BF958930
DEFINITION PM1-NN1200-011200-009-g08 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF958930
VERSION BF958930.1 GI:12376205
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 184)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=PM1&t2=PM1-NN1200-
011200-009-g08&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 184.

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FEATURES
source      Location/Qualifiers
            1. 184
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="NN1200"
            /dev_stage="Adult"
            /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the puc 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT      47 a      36 c      61 g      40 t
ORIGIN

Query Match      100.0%; Score 21; DB 10; Length 184;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 cagcagcagagcttcacat 21
        |||
Db      46 cagcagcagagcttcacat 26

RESULT 12
BI036860/c      185 bp      mRNA      linear      EST 14-JUN-2001
LOCUS      BI036860
DEFINITION      MR4-NT0140-080101-209-c09 NT0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BI036860
VERSION      BI036860.1 GI:14443486
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 185)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL      20202663
COMMENT      Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?cli=MR4&cl2=MR4-NT0140-
            080101-209-c09&cl3=2001-01-08&cl4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 134.
FEATURES
source      Location/Qualifiers
            1. 185
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="NT0140"
            /dev_stage="Adult"
            /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)

```

```

            profiles into the puc 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT      41 a      42 c      62 g      40 t
ORIGIN

Query Match      100.0%; Score 21; DB 10; Length 185;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 cagcagcagagcttcacat 21
        |||
Db      43 cagcagcagagcttcacat 23

RESULT 13
AI745406
LOCUS      AI745406      196 bp      mRNA      linear      EST 17-DEC-1999
DEFINITION      wc37401.x1 NCI-CGAP Pr28 Homo sapiens cDNA clone IMAGE:2320801 3'
            similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION      AI745406
VERSION      AI745406.1 GI:5113694
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 196)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgaps@email.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/birp/image/image.html
            Insert Length: 264 Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES
source      Location/Qualifiers
            1. 196
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="IMAGE:2320801"
            /clone_lib="NCI-CGAP_Pr28"
            /sex="male"
            /dev_stage="adult"
            /lab_host="DH10B"
            /note="Organ: prostate; Vector: p7T73D-Pac (pharmacia)
            with a modified polylinker; Plasmid DNA from the
            normalized library NCI-CGAP Pr22 was prepared, and ss
            circles were made in vitro. Following HAP purification,
            this DNA was used as tracer in a subtractive hybridization
            reaction. The driver was PCR-amplified cDNAs from a pool
            of 5,000 clones made from the same library (clonoids
            985608-986759, 1101192-1101959, and 1217928-1220615)."
            Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      39 a      60 c      35 g      62 t
ORIGIN

Query Match      100.0%; Score 21; DB 9; Length 196;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 cagcagcagagcttcacat 21
        |||

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Db 167 CAGCAGCAGAGTCTCATCAT 187

RESULT 14
BI036862/c 197 bp mRNA linear EST 14-JUN-2001

LOCUS BI036862
DEFINITION MR4-NT0140-080101-209-d10 NT0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI036862
VERSION BI036862.1 GI:14443488
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 197)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

AUTHORS
CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-NT0140-080101-209-d10&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence stop: 197.

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/organism="Homo sapiens"
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/clone_lib="NT0140"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 49 a 40 c 66 g 42 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 197;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagcttcacatc 21
|||||

Db 55 CAGCAGCAGAGTCTCATCAT 35

RESULT 15
BF957666/c 201 bp mRNA linear EST 22-JAN-2001

LOCUS BF957666
DEFINITION PM1-NN1200-251100-007-c09 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF957666
VERSION BF957666.1 GI:12374941
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 201)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

AUTHORS
CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-251100-007-c09&t3=2000-11-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 201.

FEATURES
source
1..201
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1200"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 52 a 39 c 39 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagcttcacatc 21
|||||

Db 59 CAGCAGCAGAGTCTCATCAT 39

Search completed: May 17, 2002, 15:25:36
Job time: 14513 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 15:25:46 ; Search time 147.64 Seconds
(without alignments)
66.583 Million cell updates/sec

Title: US-09-913-325-4
Perfect score: 21
Sequence: 1 cagcagcagagcttcattcatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 424068 seqs, 234053524 residues

Total number of hits satisfying chosen parameters: 848136

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq : *
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq : *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq : *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq : *
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq : *
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq : *
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	21	100.0	US-10-119-428-31	Sequence 31, App1
C 2	21	100.0	US-60-365-384-115	Sequence 115, App
C 3	16.4	78.1	US-09-930-213-252	Sequence 252, App
C 4	16.2	77.1	US-09-784-403A-6	Sequence 6, App1
C 5	16.2	77.1	US-10-126-704-12	Sequence 12, App1
C 6	16.2	77.1	US-09-540-210B-23471	Sequence 23471, A
C 7	16.2	77.1	US-09-540-210B-31214	Sequence 31214, A
C 8	16.2	77.1	US-09-975-254-17477	Sequence 17477, A
C 9	16.2	77.1	US-09-539-331D-3257	Sequence 3257, App
C 10	16.2	77.1	US-10-106-698-2234	Sequence 2234, App
C 11	16.2	77.1	US-10-099-926-918	Sequence 918, App
C 12	16.2	77.1	US-10-097-105-650	Sequence 650, App
C 13	16.2	77.1	US-10-097-105-664	Sequence 664, App
C 14	16.2	77.1	US-10-097-105-264	Sequence 264, App
C 15	16.2	77.1	US-09-954-531-790	Sequence 790, App
C 16	16.2	77.1	US-10-097-105-595	Sequence 595, App
C 17	16.2	77.1	US-09-991-150-393	Sequence 95, App
C 18	16.2	77.1	US-10-119-480-95	Sequence 95, App1
C 19	16.2	77.1	US-09-602-148A-26	Sequence 26, App1
C 20	16.2	77.1	US-09-664-249A-1	Sequence 1, App1
C 21	16.2	77.1	US-10-006-063A-335	Sequence 335, App
C 22	16.2	77.1	US-10-006-117A-335	Sequence 335, App
C 23	16.2	77.1	US-10-006-130A-335	Sequence 335, App
C 24	16.2	77.1	US-10-006-172A-335	Sequence 335, App
C 25	16.2	77.1	US-10-006-768A-335	Sequence 335, App
C 26	16.2	77.1	US-10-017-527A-335	Sequence 335, App

C 27	16.2	77.1	US-10-017-610A-335	Sequence 335, App
C 28	16.2	77.1	US-10-006-041A-335	Sequence 335, App
C 29	16.2	77.1	US-10-006-818A-335	Sequence 335, App
C 30	16.2	77.1	US-10-012-121A-335	Sequence 335, App
C 31	16.2	77.1	US-10-015-386A-335	Sequence 335, App
C 32	16.2	77.1	US-10-015-387A-335	Sequence 335, App
C 33	16.2	77.1	US-10-013-907A-335	Sequence 335, App
C 34	16.2	77.1	US-10-013-907A-335	Sequence 335, App
C 35	16.2	77.1	US-10-015-499A-335	Sequence 335, App
C 36	16.2	77.1	US-10-017-867A-335	Sequence 335, App
C 37	16.2	77.1	US-60-365-384-399	Sequence 399, App
C 38	16.2	77.1	US-10-126-704-4	Sequence 4, App1
C 39	16.2	77.1	US-09-540-209B-3032	Sequence 3032, App
C 40	16.2	77.1	US-09-053-375B-651	Sequence 651, App
C 41	15.8	75.2	US-10-106-698-2003	Sequence 2003, App
C 42	15.8	75.2	US-09-053-375B-651	Sequence 651, App
C 43	15.8	75.2	US-09-053-375B-93	Sequence 93, App1
C 44	15.8	75.2	US-10-117-982-117	Sequence 117, App
C 45	15.8	75.2	US-10-117-982-117	Sequence 117, App

ALIGNMENTS

```
RESULT 1
US-10-119-428-31/c
; Sequence 31, Application US/10119428
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Wehman, Tom
; APPLICANT: Ren, Feiyang
; APPLICANT: Ma, Yungting
; APPLICANT: Zhou, Ping
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 789CIP2
; CURRENT APPLICATION NUMBER: US/10/119,428
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 09/574,454
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: pt_FL-genes Version 1.0
; SEQ ID NO 31
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(1465)
; US-10-119-428-31

Query Match 100.0% Score 21; DB 6; Length 1614;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcagcagagcttcattcatc 21
|||
Db 136 cagcagcagagcttcattcatc 116

RESULT 2
US-60-365-384-115/c
```

; Sequence 115, Application US/60365384
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-ru
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Weinman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Zhao, Qing A.
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aiding J.
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunru
; APPLICANT: Wang, Gezh
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 814
; CURRENT APPLICATION NUMBER: US/60/365,384
; CURRENT FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PE_FL_genes Version 6.0
; SEQ ID NO 115
; LENGTH: 1839
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (132)..(1316)
; US-60-365-384-115

Query Match 100.0%; Score 21; DB 7; Length 1839;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cagcagcagagctctcatcat 21
|||||
DB 152 CAGCAGCAGAGCTTCTCATCAT 132

RESULT 3
; Sequence 252, Application US/09930213
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHE-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLMGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SERS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 252
; LENGTH: 3380
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-930-213-252

Query Match 78.1%; Score 16.4; DB 5; Length 3380;
Best Local Similarity 94.4%; Pred. No. 73;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 agcagcagagctctcatc 19
|||||
DB 190 AACAGCAGAGCTTCTCATC 173

RESULT 4
; Sequence 6, Application US/09784403A
; GENERAL INFORMATION:
; APPLICANT: Barbour, Eric
; APPLICANT: Eucilaire Meyer, Terry
; APPLICANT: Eid Saad, Mohammed
; TITLE OF INVENTION: Novel Maize Promoters
; FILE REFERENCE: 35718/208067
; CURRENT APPLICATION NUMBER: US/09/784,403A
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/107,201
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 60/103,294
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 09/410,935
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gene specific primer 1 for Gcs-2
; US-09-784-403A-6

Query Match 77.1%; Score 16.2; DB 5; Length 32;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 cagcagcagagctctcatcat 21
|||||
DB 3 cagcagcagagctctcatcat 23

RESULT 5
; Sequence 12, Application US/10126704
; GENERAL INFORMATION:
; APPLICANT: Bouguetelret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: 44.US.DIV
; CURRENT APPLICATION NUMBER: US/10/126,704
; CURRENT FILING DATE: 2002-04-20
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 12
; LENGTH: 139
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-126-704-12

Query Match 77.1%; Score 16.2; DB 6; Length 139;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 cagcagcagagctctcatcat 21
|||||

Db 3 cagaggaagagcttcacatc 23

RESULT 6
US-09-540-210B-23471
; Sequence 23471, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullishy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540, 210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972, 899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395, 244
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722, 922
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 60/005, 526
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 08/824, 029
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 60/014, 010
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826, 847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015, 533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/903, 555
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023, 308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/862, 178
; PRIOR FILING DATE: May 22, 1997
; PRIOR APPLICATION NUMBER: 60/018, 217
; PRIOR FILING DATE: May 23, 1996
; PRIOR APPLICATION NUMBER: 08/881, 589
; PRIOR FILING DATE: June 24, 1997
; PRIOR APPLICATION NUMBER: 60/021, 275
; PRIOR FILING DATE: June 25, 1996
; PRIOR APPLICATION NUMBER: 08/903, 802
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023, 308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/905, 881
; PRIOR FILING DATE: August 1, 1997
; PRIOR APPLICATION NUMBER: 60/025, 204
; PRIOR FILING DATE: August 1, 1996
; PRIOR APPLICATION NUMBER: 08/903, 471
; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025, 478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903, 556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025, 217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937, 142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026, 598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960, 746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030, 144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826, 847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015, 533
; PRIOR FILING DATE: April 10, 1996

;; PRIOR APPLICATION NUMBER: 08/755, 524
;; PRIOR FILING DATE: November 22, 1996
;; PRIOR APPLICATION NUMBER: 60/007, 495
;; PRIOR FILING DATE: November 22, 1995
;; PRIOR APPLICATION NUMBER: 09/021, 031
;; PRIOR FILING DATE: February 10, 1998
;; PRIOR APPLICATION NUMBER: 60/039, 325
;; PRIOR FILING DATE: February 13, 1997
;; PRIOR APPLICATION NUMBER: 09/035, 172
;; PRIOR FILING DATE: March 4, 1998
;; PRIOR APPLICATION NUMBER: 60/040, 431
;; PRIOR FILING DATE: March 5, 1997
;; PRIOR APPLICATION NUMBER: 09/041, 894
;; PRIOR FILING DATE: March 12, 1998
;; PRIOR APPLICATION NUMBER: 60/040, 199
;; PRIOR FILING DATE: March 14, 1997
;; PRIOR APPLICATION NUMBER: 09/050, 817
;; PRIOR FILING DATE: March 30, 1998
;; PRIOR APPLICATION NUMBER: 60/043, 792
;; PRIOR FILING DATE: April 11, 1997
;; PRIOR APPLICATION NUMBER: 09/074, 999
;; PRIOR FILING DATE: May 8, 1998
;; PRIOR APPLICATION NUMBER: 60/048, 431
;; PRIOR FILING DATE: May 29, 1997
;; PRIOR APPLICATION NUMBER: 09/107, 592
;; PRIOR FILING DATE: June 30, 1998
;; PRIOR APPLICATION NUMBER: 60/052, 751
;; PRIOR FILING DATE: July 1, 1997
;; PRIOR APPLICATION NUMBER: 09/094, 079
;; PRIOR FILING DATE: June 9, 1998
;; PRIOR APPLICATION NUMBER: 60/049, 975
;; PRIOR FILING DATE: June 13, 1997
;; NUMBER OF SEQ ID NOS: 35654
;; SOFTWARE: PERL Program
;; SEQ ID NO: 23471
;; LENGTH: 235
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; OTHER INFORMATION: Incyte ID No: hu00253322
US-09-540-210B-23471

Query Match 77.1%; Score 16.2; DB 5; length 235;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 cagcagcagagcttcacatc 21
Db 160 cagcagcagagcttcacatc 180

RESULT 7
US-09-540-210B-31214/C
; Sequence 31214, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullishy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540, 210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972, 899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395, 244
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722, 922
; PRIOR FILING DATE: September 27, 1996

```

PRIOR APPLICATION NUMBER: 60/005,526
PRIOR FILING DATE: September 29, 1995
PRIOR APPLICATION NUMBER: 08/824,029
PRIOR FILING DATE: March 25, 1997
PRIOR APPLICATION NUMBER: 60/014,010
PRIOR FILING DATE: March 25, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/903,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: 60/030,144
PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996
PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998
PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431

```

```

PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO: 31214
LENGTH: 256
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00338737
US-09-540-210B-31214

```

```

Query Match          77.1%; Score 16.2; DB 5; Length 256;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

```

```

Qy      1 cagcagcagagcttcacat 21
Db      64 CTGCATCAGAGCTTCACCT 44

```

```

RESULT      8
US-09-975-254-17477/c
; Sequence 17477, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 17477
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700954386H1
US-09-975-254-17477

```

```

Query Match          77.1%; Score 16.2; DB 5; Length 257;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

```

```

Qy      1 cagcagcagagcttcacat 21
Db      253 CAGCAGCAGAGGTTGCATCAT 233

```

```

RESULT      9
US-09-539-331D-3257/c
; Sequence 3257, Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE

```



```

1 FILE REFERENCE: PD-1022 CIP
2 CURRENT APPLICATION NUMBER: US/09/539,331D
3 CURRENT FILING DATE: 2000-03-30
4 Prior Application removed - See File Wrapper or Palm
5 NUMBER OF SEQ. ID NOS: 40961
6 SOFTWARE: PERL Program
7 SEQ ID NO 3257
8 LENGTH: 292
9 TYPE: DNA
10 ORGANISM: Homo sapiens
11 FEATURE:
12 NAME/KEY: misc.feature
13 OTHER INFORMATION: Incyte ID No: hu00740013
14 FEATURE:
15 NAME/KEY: unsure
16 LOCATION: 14-15, 54, 113-114
17 OTHER INFORMATION: a, t, c, g, or other
18 US-09-539-331D-3257

```

Query Match	77.1%	Score 16.2	DB 5	Length 292
-Best Local Similarity	85.7%	Pred. No. 72		
Matches 18; Conservative	0	Mismatches 3	Indels 0	Gaps 0

Dy 1 cagcagcagagtcttcacat 21
148 CTGCATCAGAGTCTTCATCCT 128

```

RESULT 10
US-10-106-698-2234/C
; Sequence 2234, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2234
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (305)..(305)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-2234

```

Query Match	77.18;	Score 16.2;	DB 6;	Length 319;
Best Local Similarity	85.78;	Pred. No. 73;		
Matches 18; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

```
QY      1  cagcagcagagtcctcatcat 21
          ||| | | | | | | | | | |
Db      102 CATCTGAAGAGTCTTCATCAT 82
```

RESULT 11
US-10-099-926-918
; Sequence 918, Application US/10099936
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun

```

? APPLICANT: Secrist, Heather
? APPLICANT: Jiang, Yugu
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
? FILE REFERENCE: 210121.54752
? CURRENT APPLICATION NUMBER: US/10/099,926
? CURRENT FILING DATE: 2002-03-17
? NUMBER OF SEQ ID NOS: 1982
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 918
? LENGTH: 324
? TYPE: DNA
? ORGANISM: Homo sapiens
? OS-10-099-926-918

```

Query Match	77.18;	Score 16.2;	DB 6;	Length 324;
Best Local Similarity	85.78;	Pred. No. 73;		
Matches 18; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 1 cagcagcagagtcttcattcat 21
|| ||||| | |||||
Db 143 caccagcagagccattcatcat 163

```

RESULT 12
US-10-097-105-650/c
; Sequence 650, Application US/10097105
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon E.
; APPLICANT: Secrist, Heather
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 20121.504CI
; CURRENT APPLICATION NUMBER: US/10/097,105
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 1562
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 650
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-105-650

```

Query Match	77.1%;	Score 16.2;	DB 6;	Length 325;
Best Local Similarity	85.7%;	Pred. No. 73;		
Matches 18; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 1 cagcagcaggtcttcacat 21
 ||| ||||| | |||||
Db 183 CACCAGCAGAGCCATCATCAT 163

```

RESULT 13
US-10-097-105-664/C
: Sequence 664: Application US/10097105
: GENERAL INFORMATION:
: APPLICANT: Meagher, Madeleine Joy
: APPLICANT: King, Gordon E.
: APPLICANT: Secrist, Heather
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Xu, Jiangshun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
: FILE REFERENCE: 210121.504C1
: CURRENT APPLICATION NUMBER: US/10/097,105
: CURRENT FILING DATE: 2002-03-13
: NUMBER OF SEQ ID NOS: 1562
: SOFTWARE: FASTSEQ for Windows Version 4.0

```

```

; SEQ ID NO 664
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-105-664

```

```

Query Match          77.1%; Score 16.2; DB 6; Length 330;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 cagcagcagagcttcacatc 21
    ||||||||| | |||||||
Db 184 CACGACGAGCATCATCAT 164

```

```

RESULT 14
US-10-097-105-264
; Sequence 264; Application US/10097105
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon E.
; APPLICANT: Secrist, Heather
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.504C1
; CURRENT APPLICATION NUMBER: US/10/097,105
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 1562
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 139, 218, 223, 261, 398
; OTHER INFORMATION: n = A,T,C or G
US-10-097-105-264

```

```

Query Match          77.1%; Score 16.2; DB 6; Length 409;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy- 1 cagcagcagagcttcacatc 21
     ||||||||| | |||||||
Db 143 cagcagcagagcttcacatc 163

```

```

RESULT 15
US-09-954-531-790
; Sequence 790; Application US/09954531
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392

```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 790
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-790

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Query Match          77.1%; Score 16.2; DB 5; Length 412;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 cagcagcagagcttcacatc 21
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Db 282 caatgcagagcttcacatc 302

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Search completed: May 17, 2002, 17:56:43
Job time: 9177 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 14:24:53 ; Search time 5965.48 Seconds
(without alignments)
76.160 Million cell updates/sec

Title: US-09-913-325-4
Perfect score: 21
Sequence: 1 cagcagcagcttcacatc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues
Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/2/pna/US0061_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US0062_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US0071_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US0080_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US0081_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US0082_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US0083_COMB.seq:*

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2	21	100.0	21	100.0	21	34	US-09-944-326-4	Sequence 4, Appl1	
3	21	100.0	21	100.0	21	35	US-10-080-794-4	Sequence 4, Appl1	
4	21	100.0	21	100.0	21	37	US-09-534-840-10325	Sequence 10325, A	
5	21	100.0	21	100.0	177	20	US-09-534-840-10415	Sequence 10415, A	
6	21	100.0	21	100.0	181	8	US-08-485-657-19	Sequence 19, Appl1	
7	21	100.0	21	100.0	181	17	US-09-366-380-19	Sequence 10784, A	
8	21	100.0	21	100.0	190	20	US-09-534-840-10784	Sequence 9748, Ap	
9	21	100.0	21	100.0	192	20	US-09-534-840-9748	Sequence 14, Appl1	
10	21	100.0	21	100.0	195	8	US-08-485-657-14	Sequence 9752, Ap	
11	21	100.0	21	100.0	195	17	US-09-366-380-14	Sequence 1091, Ap	
12	21	100.0	21	100.0	199	20	US-09-534-840-9752	Sequence 9505, Ap	
13	21	100.0	21	100.0	200	14	US-09-021-031-1091	Sequence 10316, A	
14	21	100.0	21	100.0	200	14	US-09-534-840-9505	Sequence 9756, Ap	
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16	21	100.0	21	100.0	203	20	US-09-534-840-10316	Sequence 9756, Ap	
17	21	100.0	21	100.0	205	20	US-09-534-840-9756	Sequence 10340, A	
18	21	100.0	21	100.0	209	20	US-09-534-840-10340	Sequence 10381, A	
19	21	100.0	21	100.0	210	20	US-09-534-840-10381	Sequence 1516, Ap	
20	21	100.0	21	100.0	213	13	US-08-918-181-1516	Sequence 1516, Ap	
21	21	100.0	21	100.0	213	20	US-09-534-840-9416	Sequence 1516, Ap	
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26	21	100.0	21	100.0	223	13	US-09-534-840-10438	Sequence 9461, Ap	
27	21	100.0	21	100.0	226	20	US-08-961-526-363	Sequence 10349, A	
28	21	100.0	21	100.0	226	20	US-09-534-840-9461	Sequence 10374, A	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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PCT-US00-04875-4
; Sequence 4, Application PC/TUS0004875
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: ANTISENSE THERAPY FOR CANCER
; FILE REFERENCE: UBC.P-020-WO
; CURRENT APPLICATION NUMBER: PCT/US00/04875
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121,726
; EARLIER FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
PCT-US00-04875-4
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Query Match 100.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cagcagcagagcttcacatc 21
Db 1 cagcagcagagcttcacatc 21
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RESULT 2
US-09-913-325-4
; Sequence 4, Application US/09913325
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-WO
; CURRENT APPLICATION NUMBER: US/09/913,325
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
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; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-913-325-4
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Query Match 100.0%; Score 21; DB 34; Length 21;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 cagcagcagagcttcacatc 21
Db 1 cagcagcagagcttcacatc 21
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RESULT 3
US-09-944-326-4
; Sequence 4, Application US/09944326
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4
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Query Match 100.0%; Score 21; DB 35; Length 21;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 cagcagcagagcttcacatc 21
Db 1 cagcagcagagcttcacatc 21
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US-10-080-794-4
; Sequence 4, Application US/10080794
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
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LENGTH: 21
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-4

Query Match 100.0%; Score 21; DB 37; Length 21;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagctctcatcat 21
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Db 1 cagcagcagagctctcatcat 21

RESULT 5
US-09-534-840-10325/c
Sequence 10325, Application US/09534840
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLEC
FILE REFERENCE: PD-1010 CIP
CURRENT APPLICATION NUMBER: US/09/534,840
CURRENT FILING DATE: 1992-07-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 13675
SOFTWARE: PERL Program
SEQ ID NO 10325
LENGTH: 177
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01113942
US-09-534-840-10325

Query Match 100.0%; Score 21; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagctctcatcat 21
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Db 88 CAGCAGCAGAGCTCTTCATCAT 68

RESULT 6
US-09-534-840-10415/c
Sequence 10415, Application US/09534840
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLEC
FILE REFERENCE: PD-1010 CIP
CURRENT APPLICATION NUMBER: US/09/534,840
CURRENT FILING DATE: 1992-07-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 13675
SOFTWARE: PERL Program
SEQ ID NO 10415
LENGTH: 177
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01055183
NAME/KEY: unsure
LOCATION: 17, 40
OTHER INFORMATION: a, t, c, g, or other
US-09-534-840-10415

Query Match 100.0%; Score 21; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagctctcatcat 21
|||||
Db 88 CAGCAGCAGAGCTCTTCATCAT 68

RESULT 7
US-08-485-657-19/c
Sequence 19, Application US/08485657
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/199,900
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-485-657-19

Query Match 100.0%; Score 21; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagctctcatcat 21
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Db 73 CAGCAGCAGAGCTCTTCATCAT 53

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RESULT 8
US-09-366-380-19/c
; Sequence 19, Application US/09366380
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-366-380-19

Query Match 100.0%; Score 21; DB 17; Length 181;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagcttcctcatc 21
Db 73 CAGCAGCAGAGCTTCATCAT 53
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RESULT 9
US-09-534-840-10784/c
; Sequence 14, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; Prior application data removed - consult PALM or file wrapper

RESULT 10
US-09-534-840-9748/c
; Sequence 9748, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Selthamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Mullaly, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MO
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 9748
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: hu01285157
US-09-534-840-9748

Query Match 100.0%; Score 21; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagcttcctcatc 21
Db 157 CAGCAGCAGAGCTTCATCAT 137

RESULT 11
US-08-485-657-14/c
; Sequence 14, Application US/08485657
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; Prior application data removed - consult PALM or file wrapper
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; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-485-657-14

Query Match          100.0%; Score 21; DB 8; Length 195;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagcttcctcatc 21
    |||
Db 87 CAGCAGCAGAGCTTCATCAT 67

RESULT 12
US-09-366-380-14/c
; Sequence 14, Application US/09366380
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
;
;
```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-366-380-14

Query Match          100.0%; Score 21; DB 17; Length 195;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagcttcctcatc 21
    |||
Db 87 CAGCAGCAGAGCTTCATCAT 67

RESULT 13
US-09-534-840-9752/c
; Sequence 9752, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Sellhammer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Muliahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MO
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEO ID NO 9752
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01227727
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
; US-09-534-840-9752

Query Match          100.0%; Score 21; DB 20; Length 199;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagcttcctcatc 21
    |||
Db 87 CAGCAGCAGAGCTTCATCAT 67

RESULT 14
US-09-021-031-1091/c
; Sequence 1091, Application US/09021031
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
;
;
```

```

; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: BLADDER CARCINOMA
; NUMBER OF SEQUENCES: 1882
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,031
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/039,325
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0319P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 853-0535
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 1091:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 2807488H1
;
; US-09-021-031-1091

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Query Match          100.0%; Score 21; DB 14; Length 200;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cagcagcagagctctcatcat 21
Db 80 CAGCAGCAGAGCTCTCATCAT 60

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RESULT 15
US-09-534-840-9505/C
; Sequence 9505, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLBO
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 9505
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu00709579
; NAME/KEY: unsure
; LOCATION: 86, 142, 156, 186
; OTHER INFORMATION: a, t, c, g, or other
;
; US-09-534-840-9505

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```

Query Match          100.0%; Score 21; DB 20; Length 200;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cagcagcagagctctcatcat 21
Db 80 CAGCAGCAGAGCTCTCATCAT 60

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Search completed: May 17, 2002, 17:56:00
Job time: 12667 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 12:33:46 ; Search time 111.1 Seconds
(without alignments)
46.429 Million cell updates/sec

Title: US-09-913-325-4

Perfect score: 21

Sequence: 1 cagcagcagcgtcttcatacat 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	181	US-08-485-657A-19	Sequence 19, Appl
2	21	100.0	181	PCR-US95-02303-18	Sequence 18, Appl
3	21	100.0	195	US-08-485-657A-14	Sequence 14, Appl
4	21	100.0	195	PCR-US95-02303-14	Sequence 14, Appl
5	17.4	82.9	633	US-08-950-925-1	Sequence 1, Appl
6	17.4	82.9	651	US-08-961-858-1	Sequence 1, Appl
7	17.4	82.9	651	US-08-961-858-3	Sequence 3, Appl
8	17.4	82.9	651	US-09-089-593-1	Sequence 1, Appl
9	17.4	82.9	651	US-09-089-593-3	Sequence 3, Appl
10	17.4	82.9	651	US-08-993-380-5	Sequence 5, Appl
11	17.4	82.9	1173	US-08-993-380-3	Sequence 3, Appl
12	16.8	80.0	330	US-08-980-060-9	Sequence 9, Appl
13	16.8	80.0	330	US-09-307-185-9	Sequence 9, Appl
14	16.8	80.0	334	US-09-307-185-90	Sequence 90, Appl
15	16.8	80.0	1806	US-08-980-060-1	Sequence 1, Appl
16	16.8	80.0	1806	US-09-307-185-1	Sequence 1, Appl
17	16.8	80.0	3459	US-08-980-060-3	Sequence 3, Appl
18	16.8	80.0	3459	US-09-307-185-3	Sequence 3, Appl
19	16.4	78.1	1051	US-09-008-697A-21	Sequence 21, Appl
20	16.2	77.1	497	US-09-247-155-41	Sequence 41, Appl
21	16.2	77.1	550	US-08-998-416-148	Sequence 148, App
22	16.2	77.1	688	PCR-US93-11310-9	Sequence 9, Appl
23	16.2	77.1	688	PCR-US93-11310-9	Sequence 9, Appl
24	16.2	77.1	975	5340934-10	Patent No. 5340934
25	16.2	77.1	975	5340934-9	Patent No. 5340934
26	16.2	77.1	1677	US-08-684-101-1	Sequence 1, Appl
27	16.2	77.1	1677	US-09-205-814-1	Sequence 1, Appl

28	15.8	75.2	361	4	US-09-387-212-5	Sequence 5, Appl
29	15.8	75.2	2674	4	US-09-817-180-1	Sequence 1, Appl
30	15.8	75.2	15297	4	US-09-817-180-3	Sequence 3, Appl
31	15.4	73.3	45	1	US-07-885-689A-7	Sequence 7, Appl
32	15.4	73.3	576	1	US-07-885-689A-28	Sequence 28, Appl
33	15.4	73.3	576	1	US-08-093-383-4	Sequence 4, Appl
34	15.4	73.3	579	1	US-07-885-689A-35	Sequence 35, Appl
35	15.4	73.3	579	1	US-07-885-689A-37	Sequence 37, Appl
36	15.4	73.3	600	6	5514646-37	Patent No. 5514646
37	15.4	73.3	601	1	US-07-764-655D-6	Sequence 6, Appl
38	15.4	73.3	601	1	US-07-801-164A-3	Sequence 3, Appl
39	15.4	73.3	603	1	US-07-764-655D-7	Sequence 7, Appl
40	15.2	72.4	423	1	US-08-470-179-35	Sequence 35, Appl
41	15.2	72.4	423	1	US-08-470-179-51	Sequence 51, Appl
42	15.2	72.4	423	1	US-08-470-179-53	Sequence 53, Appl
43	15.2	72.4	423	1	US-08-470-179-76	Sequence 76, Appl
44	15.2	72.4	423	1	US-08-470-179-80	Sequence 80, Appl
45	15.2	72.4	423	1	US-08-470-179-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-08-485-657A-19/c
; Sequence 19, Application US/08485657A
; Patent No. 5942389
GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; FAX:
INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-485-657A-19

Query Match 100.0%; Score 21; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cagcagcagcgtcttcatacat 21

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Db      73 CAGCAGCAGAGTCTTCATCAT 53
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RESULT 2
PCT-US95-02303-18/C
; Sequence 18, Application PC/TUS9502303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: With Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02303
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-02303-18

Query Match      100.0%; Score 21; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 21; Conservative 0; Indels 0; Gaps 0;

QY      1 cagcagcagagcttcacat 21
      |||||||
Db      73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 3
US-08-485-657A-14/C
; Sequence 14, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: With Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-485-657A-14

Query Match      100.0%; Score 21; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 cagcagcagagcttcacat 21
      |||||||
Db      87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 5
US-08-950-925-1/C
; Sequence 1, Application US/08950925
; Patent No. 6072040
; GENERAL INFORMATION:
; APPLICANT: Dave, Kirti I.
; APPLICANT: Botvanszki, Janos
; APPLICANT: Sitar, Eva
; TITLE OF INVENTION: Stabilized Conjugates of Uncomplexed
; TITLE OF INVENTION: Subunits of Multimeric Proteins
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,925
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Axford, Laurie A
; REGISTRATION NUMBER: 35,053
; REFERENCE/DOCKET NUMBER: 32260-20004.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..630
; OTHER INFORMATION:
;
US-08-950-925-1

Query Match      82.9%; Score 17.4; DB 3; Length 633;
Best Local Similarity 94.7%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 cagcagcagagcttcac 19
        |||
DB      162 CAGCAGCAGAGCTTCAGC 144

RESULT 6
US-08-961-858-1/C
; Sequence 1, Application US/08961858
; Patent No. 5834210
; GENERAL INFORMATION:
; APPLICANT: Liu, Shigui
; APPLICANT: Shi, Qiuwei
; TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauder & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,858
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
```

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;
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
;
US-08-961-858-1
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```

Query Match      82.9%; Score 17.4; DB 2; Length 651;
Best Local Similarity 94.7%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

QY      1 cagcagcagagcttcac 19
        |||
DB      180 CAGCAGCAGAGCTTCAGC 162
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```

RESULT 7
US-08-961-858-3/C
; Sequence 3, Application US/08961858
; Patent No. 5834210
; GENERAL INFORMATION:
; APPLICANT: Liu, Shigui
; APPLICANT: Shi, Qiuwei
; TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauder & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,858
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: native form
; HYPOTHETICAL: NO
;
US-08-961-858-3
```

```

Query Match      82.9%; Score 17.4; DB 2; Length 651;
Best Local Similarity 94.7%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

QY      1 cagcagcagagcttcac 19
        |||
DB      180 CAGCAGCAGAGCTTCAGC 162
```

RESULT 8
US-09-089-593-1/C
; Sequence 1, Application US/09089593
; Patent No. 6060278
; GENERAL INFORMATION:
; APPLICANT: Liu, Shigui
; APPLICANT: Shi, Qianwei
; TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/089,593
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,858
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; US-09-089-593-1

Query Match 82.9%; Score 17.4; DB 3; Length 651;
Best Local Similarity 94.7%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cagcagcagagcttcac 19
|||||
Db 180 CAGCAGCAGAGCTTCACG 162

RESULT 9
US-09-089-593-3/C
; Sequence 3, Application US/09089593
; Patent No. 6060278
; GENERAL INFORMATION:
; APPLICANT: Liu, Shigui
; APPLICANT: Shi, Qianwei
; TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/089,593
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,858
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: native form
; US-09-089-593-3

Query Match 82.9%; Score 17.4; DB 3; Length 651;
Best Local Similarity 94.7%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cagcagcagagcttcac 19
|||||
Db 180 CAGCAGCAGAGCTTCACG 162

RESULT 10
US-08-993-380-5/C
; Sequence 5, Application US/08993380B
; Patent No. 6077676
; GENERAL INFORMATION:
; APPLICANT: Shi, Qianwei
; APPLICANT: Song, Qian-Li
; TITLE OF INVENTION: SINGLE CHAIN POLYPEPTIDES COMPRISING TROPONIN I AND
; FILE REFERENCE: 1112-1-053
; CURRENT APPLICATION NUMBER: US/08/993,380B
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens (modified)
; US-08-993-380-5

Query Match 82.9%; Score 17.4; DB 3; Length 651;
Best Local Similarity 94.7%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cagcagcagagcttcac 19
|||||
Db 180 CAGCAGCAGAGCTTCACG 162

RESULT 11
US-08-993-380-3/C

; Sequence 3, Application US/08993380B
; Patent No. 6077676
; GENERAL INFORMATION:
; APPLICANT: Shi, Qianwei
; APPLICANT: Song, Qianli
; TITLE OF INVENTION: SINGLE CHAIN POLYPEPTIDES COMPRISING TROPONIN C
; TITLE OF INVENTION: TROPONIN C
; FILE REFERENCE: 1112-1-053
; CURRENT APPLICATION NUMBER: US/08/993,380B
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens (modified)
US-08-993-380-3

* Query Match 82.9%; Score 17.4; DB 3; Length 1173;
Best Local Similarity 94.7%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cagcagcagatctcatc 19
|||||
DB 162 CAGCAGCAGAGCTTCACG 144

RESULT 12
US-08-980-060-9/C
; Sequence 9, Application US/08980060
; Patent No. 5965421
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: FENG, PING
; APPLICANT: MUZIO, MARTA
; APPLICANT: DIXIT, VISHVA M.
; TITLE OF INVENTION: HUMAN IRAK-2
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,060
; FILING DATE: Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-980-060-9

Query Match 80.0%; Score 16.8; DB 2; Length 330;

Best Local Similarity 90.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 agcagcagatctcatcat 21
|||||
DB 111 AGCAGGTGAGCTTCATCAT 92

RESULT 13
US-09-307-185-9/C
; Sequence 9, Application US/09307185
; Patent No. 6222019
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: FENG, PING
; APPLICANT: MUZIO, MARTA
; APPLICANT: DIXIT, VISHVA M.
; TITLE OF INVENTION: HUMAN IRAK-2
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,185
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,060
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-307-185-9

Query Match 80.0%; Score 16.8; DB 4; Length 330;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 agcagcagatctcatcat 21
|||||
DB 111 AGCAGGTGAGCTTCATCAT 92

RESULT 14
US-09-227-357-90/C
; Sequence 90, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357

```

CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 334
TYPE: DNA
ORGANISM: Homo sapiens

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FEATURE:
NAME/KEY: SITE
LOCATION: (321)
OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-90

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Query Match      80.0%; Score 16.8; DB 4; Length 334;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2  accagcagagcttcacat 21
Db      95  accagcagagcttcacat 76

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RESULT 15
US-08-980-060-1/c
Sequence 1, Application US/08980060
Patent No. 5965421
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1806 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1803
US-08-980-060-1

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```

Query Match      80.0%; Score 16.8; DB 2; Length 1806;
Best Local Similarity 90.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2  accagcagagcttcacat 21
Db      1157  accagcagagcttcacat 1138

```

Mon May 20 10:17:54 2002

us-09-913-325-4.rni

Page 7

Search completed: May 17, 2002, 16:06:10
Job time: 12744 sec

PS Claim 3; Page 36; 38pp; English.

XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2), also known as
CC clusterin, sulfated glycoprotein-2 or SCP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed
CC at human TRPM-2 can be used in the treatment of tumour cells expressing
CC the TRPM-2 gene. These include prostate cancer, renal cell cancer and
CC some breast cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective.

XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagctctcatcat 21
Db 1 cagcagcagagctctcatcat 21

RESULT 2

AAT00416/c
ID AAT00416 standard; cDNA; 195 BP.

XX AAT00416;

AC AAT00416;

XX 26-MAR-1996 (first entry)

DE Genetic suppressor element HL7.1.

XX Genetic suppressor element; GSE; platinum-based drug; cisplatin;
KM chemotherapy; HL7.1; testosterone-repressed prostatic message-2; TRPM-2;

XX Synthetic.

XX WO9522612-A2.

XX 24-AUG-1995.

XX 22-FEB-1995; 95MO-US02303.

XX 22-FEB-1994; 94US-0199900.

XX (UNII) UNIV ILLINOIS FOUND.

XX Gudkov A, Kirschling DJ, Roninson IB;

XX WPI; 1995-302718/39.

PT Genetic suppressor elements which confer resistance to
PT platinum-based drugs, eg. cisplatin, on cancer cells - useful for
PT enhancement of chemotherapy, and for diagnosis of resistance to
PT these drugs.

XX Claim 14; Fig 17; 75pp; English.

CC The sequences represented by AAT00405-T00418 are genetic suppressor
CC elements (GSEs). This sequence represents GSE HL6.10. This sequence
CC shows homology to the cDNA encoding testosterone-repressed prostatic
CC message-2 (TRPM-2). These sequences were obtained from a cDNA library
CC derived from the total cDNA of a cisplatin sensitive cell. Genetic
CC suppressor elements confer resistance to platinum-based drugs (Pds),
CC such as cisplatin. These functional GSEs can then be used to create
CC probes for the parent gene. The probes can then be used in a method of
CC measuring the level of GSE gene expression. The GSEs can be used in
CC methods of diagnosis of resistance to Pds by measuring the level of
CC expression of GSE genes. The GSEs are also used in methods to overcome
CC resistance to Pds in cancer cells. The GSEs (or fragments of them) can

CC be used to inhibit the function of genes associated with sensitivity to
CC Pds. For enhancement of chemotherapy, a GSE can be transferred (either
CC alone or with another gene) on an expression vector into blood
CC progenitor cells from a cancer patient. The cells are returned to the
CC patients circulation and allowed to repopulate the blood before
CC aggressive chemotherapy is carried out (using higher cisplatin
CC concentrations than normal), this will thereby avoid toxic side effects
CC to the immune system as the blood cells will be GSE resistant.

XX Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 other;

Query Match 100.0%; Score 21; DB 16; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagctctcatcat 21
Db 87 CAGCAGCAGAGCTCTCATCAT 67

RESULT 3

AAC06940/c
ID AAC06940 standard; cDNA; 275 BP.

XX AAC06940;

AC AAC06940;

XX 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 11015.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KM gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GSEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 1; SEQ ID 11015; 71pp + CD-ROM; English.

CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

XX Sequence 275 BP; 59 A; 88 C; 85 G; 43 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 275;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagcttcctcatcat 21
 |||
 DB 128 CAGCAGCAGAGCTTCATCAT 108

RESULT 4

AAf94824/C
 ID AAF94824 standard; cDNA: 396 BP.

XX AAF94824;

XX 23-MAY-2001 (first entry)

XX Human ovarian cancer associated coding sequence SEQ ID NO: 15.

XX Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

XX Homo sapiens.

XX W0200118046-A2.

XX 15-MAR-2001.

XX 08-SEP-2000; 2000WO-US24827.

XX 10-SEP-1999; 99US-0394374.

XX 01-MAY-2000; 2000US-0561778.

XX 15-AUG-2000; 2000US-0640173.

XX 07-SEP-2000; 2000US-0656668.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA;

XX WPI; 2001-211395/21.

XX Isolated polypeptides associated with ovarian carcinomas, and the

XX nucleic acids that encode them, useful for the prevention diagnosis and

XX treatment of ovarian cancers -

XX Claim 18; Page 120; 1899p; English.

XX The present invention provides a number of coding sequences and proteins,

XX the over-expression of which is associated with ovarian carcinoma/cancer.

XX These can be used in the diagnosis, treatment and prevention of ovarian

XX cancer, optionally by gene therapy or in the form of a vaccine. The

XX present sequence is an example of one of these sequences.

XX Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

QY 1 cagcagcagagcttcctcatcat 21
 |||
 DB 79 CAGCAGCAGAGCTTCATCAT 59

RESULT 5
 AAC03751/C
 ID AAC03751 standard; cDNA: 491 BP.

XX AAC03751;

XX 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 3749.
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EPI033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclet A, Giordano J;

XX WPI; 2000-500381/45.

XX P-PSDB; AAG03745.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

XX diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 1; SEQ ID 3749; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from

XX cDNAs encoding secreted proteins. An ORF has been identified within the

XX sequence. The 5' ESTs were prepared from total human RNAs or polyA RNAs

XX derived from 30 different tissues. EST sequences usually correspond

XX mainly to the 3' untranslated region (UTR) of the mRNA because they are

XX often obtained from oligo-dT primed cDNA libraries. Such ESTs are not

XX well suited for isolating cDNA sequences derived from the 5' ends of

XX mRNAs and even in those cases where longer cDNA sequences have been

XX obtained, the full 5' UTR is rarely included. 5' ESTs are derived from

XX cDNAs with intact 5' ends and can therefore be used to obtain full length

XX cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,

XX CC gene therapy and chromosome mapping procedures. They are used to obtain

XX CC upstream regulatory sequences and to design expression and secretion

XX vectors.

XX Sequence 491 BP; 149 A; 114 C; 149 G; 78 T; 1 other;

QY 1 cagcagcagagcttcctcatcat 21
 |||
 DB 128 CAGCAGCAGAGCTTCATCAT 108

RESULT 6
 AAV89150/C
 ID AAV89150 standard; cDNA: 512 BP.

XX AAV89150;

XX 15-FEB-1999 (first entry)

XX EST clone CG1.

XX Human; secreted protein; expressed sequence tag; EST; haematopoiesis;

XX tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;

XX KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;

XX gene therapy; ss.

XX Homo sapiens.

XX W09845436-A2.

XX 15-OCT-1998.
 PD Best Local Similarity 100.0%; Score 21; DB 20; Length 512;
 XX 10-APR-1998; 98WO-US06955.
 PF Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 10-APR-1997; 97US-0838821.
 PR (GENY) GENETICS INST INC.
 XX
 PA Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Werberg D;
 PI Racle LA, Spaulding V, Treacy M;
 XX WPI; 1999-070077/06.
 DR
 XX New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries.
 XX
 PS Claim 1: Page 126; 618pp; English.
 XX
 CC The present sequence represents a human expressed sequence tag (EST).
 CC The polynucleotide, which is a secreted EST, and the encoded protein
 CC are predicted to have useful biological activities which would make
 CC them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals, although no supporting data is
 CC given. Suggested activities include nutritional activity, immune
 CC stimulating or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The polynucleotide may also be useful for gene therapy.
 XX
 SQ Sequence 512 BP; 154 A; 114 C; 150 G; 94 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 512;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 cagcagcagagctctcatcat 21
 DB 55 CAGCAGCAGAGCTCTCATCAT 35
 RESULT 7
 AA42136/C
 ID AA42136 standard; CDNA: 572 BP.
 XX
 AC AA42136;
 XX
 DT 31-JAN-2000 (first entry)
 DT
 XX Human normal bladder tissue cDNA derived EST 15.
 DE
 KW Human; bladder; treatment; EST; expressed sequence tag; cytostatic;
 KW cancer; gene therapy; ss.
 OS Homo sapiens.
 XX
 PN DE19818620-A1.
 XX
 PD 28-OCT-1999.
 PF 21-APR-1998; 98DE-1018620.
 PR 21-APR-1998; 98DE-1018620.
 XX
 PF (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 PI WPI; 1999-602416/52.
 XX

XX New polypeptides and their nucleic acids, useful for treatment of
 PT bladder tumour and identification of therapeutic agents
 XX
 PS Claim 3; Page 158; 366pp; German.
 XX
 CC This invention describes novel polypeptide fragment sequences (I) and
 CC their encoding nucleic acids (II) which are highly expressed in normal
 CC bladder tissue and have cytostatic activity. (II) are used for
 CC recombinant expression of (I) and to isolate complete genes. (I) are
 CC used to identify agents suitable for the treatment of bladder tumours,
 CC to directly treat this form of cancer (including expression from gene
 CC therapy vectors), or are used in a preparation for cancer treatment. (I)
 CC is also used for the generation of specific antibodies. (II) are
 CC identified by assembling ESTs (expressed sequence tags) from a
 CC particular tissue type before comparison of expression patterns. This
 CC allows a significantly longer fragment of the gene to be revealed, and
 CC therefore reduces the number of failures because of ESTs from different
 CC libraries representing different parts of the same unknown gene
 CC distorting the estimated frequency of occurrence in a particular tissue.
 CC AA42122-242248 represent EST fragments derived from a human normal
 CC bladder tissue cDNA library which encode the protein fragments
 CC represented in AAF60329-Y60591.
 XX
 SQ Sequence 572 BP; 161 A; 128 C; 186 G; 97 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 572;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 cagcagcagagctctcatcat 21
 DB 196 CAGCAGCAGAGCTCTCATCAT 176
 RESULT 8
 AAA43857/C
 ID AAA43857 standard; CDNA: 922 BP.
 XX
 AC AAA43857;
 XX
 DT 21-AUG-2000 (first entry)
 DT
 XX Human secreted expressed sequence tag SEQ ID NO:432.
 DE
 KW Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
 KW expressed sequence tag; EST; probe; chemotactic; proliferative;
 KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
 KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
 KW antiviral; antidiabetic; antiaschmatic; vulnary; antiparkinsonian;
 KW anticancer; osteoprotective; neuroprotective; noctropic; antipsoriatic;
 KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;
 KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
 KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
 KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
 KW central nervous system disorder; Alzheimer's disease; stroke;
 KW parkinson's disease; Huntington's disease; coagulation disorder;
 KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
 KW tumour; infection; depression; psoriasis; ss.
 OS Homo sapiens.
 XX
 PN WO200021991-A1.
 XX
 PD 20-APR-2000.
 PF 15-OCT-1999; 99WO-US24206.
 PR 15-OCT-1998; 98US-0104436.
 XX
 PF (GENY) GENETICS INST INC.
 PA
 XX

PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR;
 XX WPI: 2000-317938/27.
 DR
 XX
 PT Isolated polynucleotides, and encoded proteins, comprising secreted
 PT expressed sequence tags (ESTs), useful for treating various disorders
 PT such as autoimmune, infectious, and central nervous system disorders -
 XX
 XX
 PS Claim 1: Page 316: 803pp; English.
 XX
 CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
 CC sequence tags (ESTs), isolated from human, mouse, chicken and rat
 CC tissue sources. The ESTs can have a range of activities depending on
 CC the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
 CC antiallergic; vulnerary; antiulcer; osteopathic; neuroprotective;
 CC neurotropic; antiparkinsonian; antipsoriatic; cerebroprotective;
 CC anticonvulsant; and antidepressant. The ESTs can be used for gene
 CC therapy and in vaccines. The ESTs are useful as probes for the
 CC identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the ESTs. Proteins encoded by the ESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
 CC in the exemplification of the present invention.
 XX
 XX Sequence 922 BP: 243 A; 265 C; 244 G; 166 T; 4 other;
 SQ
 Query Match 100.0%; Score 21; DB 21; Length 922;
 Best local Similarity 100.0%; Pred. No. 4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 cagcagcagagcttcacatc 21
 Db 52 CAGCAGCAGAGCTTCATCAT 32
 RESULT 9
 AAS44948/C
 ID AAS44948 standard; cDNA: 1568 BP.
 XX
 XX AAS44948;
 AC
 XX
 DT 18-DEC-2001 (first entry)
 DT
 XX
 DE cDNA encoding novel human secretory protein, Seq ID No 29.
 XX
 XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen; ss.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX

PF 05-MAR-2001; 2001WO-US04942.
 XX
 XX 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616647.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 PA
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao Q, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 XX WPI: 2001-589934/66.
 DR P-PSDB: AAU28048.
 DR
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 XX
 PS Claim 1: SEQ ID No 29; 107pp; English.
 XX
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.
 XX
 XX
 SQ Sequence 1568 BP: 386 A; 456 C; 434 G; 292 T; 0 other;
 QY
 Query Match 100.0%; Score 21; DB 22; Length 1568;
 Best local Similarity 100.0%; Pred. No. 4.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 cagcagcagagcttcacatc 21
 Db 90 CAGCAGCAGAGCTTCATCAT 70
 RESULT 10
 AAQ11503/C
 ID AAQ11503 standard; DNA: 1651 BP.
 XX

```

AC AAQ11503;
XX
XX 20-JUN-1991 (first entry)
XX
XX Cytolysis inhibitor gene.
DE
XX Cytolysis inhibitor; perforin; immunological effector molecule;
KW
XX Interfility; ss.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
XX sig_peptide 199..261
XX /*tag= a
XX mat_peptide 262..1542
XX /*tag= b
XX /product= cytolysis inhibitor
XX
XX DE3933850-A.
XX
XX 18-APR-1991.
XX
XX 06-OCT-1989; 89DE-3933850.
XX
XX 06-OCT-1989; 89DE-3933850.
XX
XX (SCHD ) SCHERING AG.
XX
XX Tschopp J, Jenne D;
XX
XX WPI: 1991-118338/17.
XX
XX DNA sequence coding for cytolysis inhibitor - is strong inhibitor
XX of terminal complement protein, e.g. perforin secreted by killer
XX cells
XX
XX Claim 2; Page 8; 15pp; German.
XX
XX Two probes were prepared based on the known partial amino acid
XX sequences of both chains of the Cytolysis inhibitor and used to
XX screen a liver-specific cDNA library. One clone which hybridised
XX positively to both probes was found to contain a 1.7kb BamHI-KpnI
XX fragment. This was inserted into plasmid pGEM4, to give pGEM4/ZI-1.
XX E.coli transformed with the plasmid are deposited under DSM # 5269.
XX The insert has the sequence given in this file.
XX
XX See also AAQ11501 and AAQ11502.
XX
XX Sequence 1651 BP; 405 A; 481 C; 447 G; 318 T; 0 other;
SQ
Query Match 100.0%; Score 21; DB 12; Length 1651;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cagcagcagagctctcatcat 21
DB 216 CAGCAGCAGAGCTCTCATCAT 196
RESULT 11
AAH23086/C
ID AAH23086 standard; DNA; 1678 BP.
XX
XX AAH23086;
AC
XX
XX 17-SEP-2001 (first entry)
XX
XX Osteoarthritis tissue-derived nucleic acid sequence #16.
DE
XX
XX Osteoarthritis; infectious disorder; Crohn's disease; sepsis; human;
XX wound healing; osteopathic; anti-arthritis; anti-inflammatory;
XX vulnerability; antibacterial; anti-allergic; ds.
XX

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OS Homo sapiens.
XX
XX WO200153531-A2.
XX
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US00016.
XX
XX 18-JAN-2000; 2000US-0176523.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Phippard D, Vasanthakumur G, Dotson S, Ma X;
XX
XX WPI: 2001-451914/48.
XX
XX Substantially purified protein, polypeptide or their fragments, used to
XX identify a biologically active compound or composition and treat
XX mammalian osteoarthritis -
XX
XX Claim 1; Page 102-103; 144pp; English.
XX
XX Sequences AAH23071-23152 represent nucleic acid sequences derived from
XX osteoarthritis tissues. The sequences are useful as probes and for the
XX diagnosis or prognosis of mammalian osteoarthritis. The polynucleotides
XX and polypeptides of the invention are useful for generating diagnostic
XX reagents, as targets for small molecule drug development, generation of
XX therapeutics, and cloning genes. Specific antibodies are used to generate
XX enzyme linked immunosorbent assays for detection of osteoarthritis. The
XX invented molecules can be used to treat osteoarthritis or to analyse the
XX disease-modifying activity of osteoarthritis drugs. Other disorders
XX treatable using the nucleic acid sequences include atopic disorders
XX and infectious disorders e.g. Crohn's disease and sepsis, and wound
XX healing.
XX
XX Sequence 1678 BP; 424 A; 491 C; 450 G; 313 T; 0 other;
SQ
Query Match 100.0%; Score 21; DB 22; Length 1678;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cagcagcagagctctcatcat 21
DB 90 CAGCAGCAGAGCTCTCATCAT 70
RESULT 12
AAH24790/C
ID AAH24790 standard; DNA; 50 BP.
XX
XX AAH24790;
AC
XX
XX 21-JUN-1999 (first entry)
XX
XX Interleukin-18 binding protein splice variant IL-18BPA PCR primer.
DE
XX
XX Interleukin-18 binding protein; IL-18BP; IL-18BPA; splice variant;
XX human; autoimmune disease; inflammation; diabetes; pancreatitis;
XX rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
XX psoriasis; inflammatory bowel disease; multiple sclerosis;
XX ischemic heart disease; ischemic brain injury; gene therapy; PCR;
XX primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9309063-A1.
XX
XX 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-IL00379.
XX

```

PR 22-JUL-1998; 98IL-0125463.
 PR 14-AUG-1997; 97IL-0121554.
 PR 27-AUG-1997; 97IL-0121639.
 PR 29-SEP-1997; 97IL-0121860.
 PR 06-NOV-1997; 97IL-0122134.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Dinarello C, Kim SH, Novick D, Rubinstein M;
 XX
 DR WPI; 1999-180975/25.
 XX
 PT New interleukin-18 binding protein - useful for treating human
 PT diseases, including autoimmune disease and inflammation
 XX
 PS Example 7; Page 39; 100pp; English.
 XX
 CC The present sequence is a reverse primer that was used with a
 CC forward primer (see AAX24754) in the PCR amplification of the coding
 CC region of a cDNA clone (see AAX24749) coding for human interleukin-18
 CC binding protein splice variant IL-18Bpa (see AAW98004). The PCR
 CC products were cut with XbaI and cloned into the XbaI site of the
 CC pEF-BOS expression vector. IL-18Bpa was expressed in transfected
 CC COS7 cells. The invention provides IL-18BP polypeptides capable of
 CC binding IL-18 and/or modulating and/or blocking IL-18 activity.
 CC These can be used to treat conditions requiring the protein
 CC (claimed), such as autoimmune diseases, type I diabetes, rheumatoid
 CC arthritis, graft rejections, inflammatory bowel disease, sepsis,
 CC multiple sclerosis, ischemic heart diseases, ischemic brain injury,
 CC chronic hepatitis, psoriasis, and chronic/acute pancreatitis.
 XX
 SQ Sequence 50 BP; 13 A; 8 C; 13 G; 16 T; 0 other;
 XX
 Query Match 84.8%; Score 17.8; DB 20; Length 50;
 Best Local Similarity 90.5%; Pred. No. 76;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 cagcagcagagcttcacatc 21
 |||||
 Db 42 CAGCAGCAGCGTCATCATCAT 22
 RESULT 13
 AAT64832/c
 ID AAT64832 standard; cDNA; 417 BP.
 XX
 AC AAT64832;
 XX
 DT 04-SEP-1997 (first entry)
 XX
 DE Coral cobra venom protein cDNA clone VI.
 XX
 KW Coral cobra; snake venom; toxin; snakebite; antidote; antiserum;
 KW immunodominant; ss.
 XX
 OS Micrurus corallinus.
 XX
 FH Key Location/Qualifiers
 FH CDS 15..251
 FT /tag= a
 FT /product= putative_toxin
 FT 15..77
 FT /tag= b
 FT /note= "deduced by comparison to homologous sequences"
 FT 401..406
 FT /tag= c
 FT 417
 FT polyA_site
 FT /tag= d
 XX
 XX BR9403020-A.
 XX
 XX 03-SEP-1996.
 XX
 PD

XX
 XX 30-AUG-1994; 94BR-0003020.
 XX
 XX 30-AUG-1994; 94BR-0003020.
 XX
 XX (BUTA-) FUNDACAO BUTANTAN.
 XX (HOPL/) HO P L.
 PA
 PI Ho PL;
 XX
 DR WPI; 1996-434245/44.
 DR P-PSDB; AAW18368.
 XX
 PT Coral cobra venom toxin cDNA - and prepn of the venom by genetic
 PT engineering or chemical synthesis for prodn. of antiserum to treat
 PT snake bites
 XX
 PS Claim 1; Fig 7(A); 16pp; Portuguese.
 XX
 CC The abundant 07 cDNAs which code for immunodominant toxins from
 CC the poison glands of the coral cobra (Micrurus corallinus) have been
 CC identified and cloned. The present sequence is that of cDNA clone
 CC VI. The sequences from clones VI, V3 and V7 (see AAT64832, AAT64833 and
 CC AAT64834) are all very similar, with V3 and V7 giving the same
 CC deduced amino acid sequence. The toxins can be used for preparing
 CC antisera to treat coral cobra bites.
 CC (N.B. The numbering shown on figure 7 gives the sequence as being
 CC 447 nucleotides long).
 XX
 SQ Sequence 417 BP; 103 A; 94 C; 91 G; 129 T; 0 other;
 XX
 Query Match 84.8%; Score 17.8; DB 17; Length 417;
 Best Local Similarity 90.5%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 cagcagcagagcttcacatc 21
 |||||
 Db 32 CAGCAGCAGAGTTCATCATCTT 12
 RESULT 14
 AAT64834/c
 ID AAT64834 standard; cDNA; 418 BP.
 XX
 AC AAT64834;
 XX
 DT 04-SEP-1997 (first entry)
 XX
 DE Coral cobra venom protein cDNA clone V7.
 XX
 KW Coral cobra; snake venom; toxin; snakebite; antidote; antiserum;
 KW immunodominant; ss.
 XX
 OS Micrurus corallinus.
 XX
 FH Key Location/Qualifiers
 FH CDS 16..252
 FT /tag= a
 FT /product= putative_toxin
 FT 16..78
 FT /tag= b
 FT /note= "deduced by comparison to homologous sequences"
 FT 402..407
 FT /tag= c
 FT 418
 FT polyA_site
 FT /tag= d
 XX
 XX BR9403020-A.
 XX
 XX 03-SEP-1996.
 XX
 XX 30-AUG-1994; 94BR-0003020.
 XX
 XX

RESULT	15
AA64833/c	
ID	AA64833 standard; cDNA; 426 BP.
XX	
XX	AA64833;
XX	
XX	04-SEP-1997 (first entry)
XX	
DE	Coral cobra venom protein cDNA clone V3.
XX	
XX	Coral cobra; snake venom; toxin; snakebite; antidote; antiserum;
KW	immunodominant; ss.
XX	
OS	Micrurus corallinus.
XX	
XX	Key
EH	Location/Qualifiers
FT	CDS
FT	24..260
FT	/*tag= a
FT	/product= putative_toxin
FT	24..86
FT	/*tag= b
FT	/note= "deduced by comparison to homologous sequences
FT	410..415
FT	/*tag= c
FT	426
FT	polyA_site
FT	/*tag= d
XX	
XX	BR9403020-A.
PN	
PN	03-SEP-1996.
XX	
XX	30-AUG-1994;
XX	94BR-0003020.
XX	
XX	30-AUG-1994.
XX	94BR-0003020.

Search completed: May 17, 2002, 16:13:54
Job time: 7046 sec

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OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 11:35:40 ; Search time 1959.41 Seconds
(without alignments)
224.280 Million cell updates/sec

Title: US-09-913-325-4
Perfect score: 21
Sequence: 1 cagcagcagagcttcacatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank1:
1: gb_da:*
2: gb_hg:*
3: gb_in:*
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6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hgt_hum:*
31: em_hgt_inv:*
32: em_hgt_other:*
33: em_hgtgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	396	6	AX093197	Sequence 15 from Patent WO0118046.
2	100.0	1648	6	HUMRPM2A	AX093197 Sequence
3	100.0	1651	6	A21577	Human TRPM-421577 blood plasma
4	100.0	1651	9	HUMCLI	M25915 Human compl
5	100.0	1658	9	BC019588	BC019588 Homo sapi
6	100.0	1676	6	HSCSP40	X14723 Human SP-40
7	100.0	1678	6	AX202086	AX202086 Sequence
8	100.0	1684	6	BC010514	BC010514 Homo sapi
9	100.0	7610	9	HUMRPM2A1	M63376 Human TRPM-421577
10	100.0	175382	2	AF235104	AF235104 Homo sapi
11	100.0	187433	2	AC025192	AC025192 Homo sapi
12	100.0	234431	9	AF311103	AF311103 Homo sapi
13	19.4	1636	4	DOGCP80	M55251 Dog g1ycop
14	19.4	92.4	4	AF118852	AF118852 Orycto1ag
15	18.4	87.6	3287	AF063235	AF063235 Pneumocys
16	18	1632	4	PICGCMRA	M84639 Pig complem
17	17.8	84.8	264	AF023271	AF023271 Naia sput
18	17.8	84.8	264	AF023272	AF023272 Naia sput
19	17.8	84.8	278	NSU86588	U86588 Naia sputat
20	17.8	84.8	278	NSU86589	U86589 Naia sputat
21	17.8	84.8	278	NSU86591	U86591 Naia sputat
22	17.8	84.8	278	NSU86592	U86592 Naia sputat
23	17.8	84.8	278	NSU86593	U86593 Naia sputat
24	17.8	84.8	278	NSU86594	U86594 Naia sputat
25	17.8	84.8	278	NSU86595	U86595 Naia sputat
26	17.8	84.8	278	NSU86596	U86596 Naia sputat
27	17.8	84.8	278	NSU86597	U86597 Naia sputat
28	17.8	84.8	283	G09801	G09801 human STS C
29	17.8	84.8	290	AF276223	AF276223 Naia sput
30	17.8	84.8	294	AF098923	AF098923 Naia sput
31	17.8	84.8	294	AF098924	AF098924 Naia sput
32	17.8	84.8	349	ALTOXD	X13372 Alpyrusus 1
33	17.8	84.8	365	AF142323	AF142323 Bungarus
34	17.8	84.8	392	DADACSCI	X53410 D.angustice
35	17.8	84.8	392	DAPLP	X52260 Dendroaspis
36	17.8	84.8	408	AF276222	AF276222 Naia sput
37	17.8	84.8	418	AF187363	AF187363 Micurus
38	17.8	84.8	420	AF197565	AF197565 Micurus
39	17.8	84.8	428	AF197564	AF197564 Micurus
40	17.8	84.8	452	BMKNCB1	X51412 Bungarus mu
41	17.8	84.8	457	LSERABUB	X16950 Laticauda s
42	17.8	84.8	477	AB015513	AB015513 Laticauda
43	17.8	84.8	480	AF026893	AF026893 Naia sput
44	17.8	84.8	483	LSERARAR	X02533 Laticauda s
45	17.8	84.8	486	MC0344067	AJ344067 Micurus

ALIGNMENTS

RESULT	1	AX093197/c	Sequence 15 from Patent WO0118046.	LOCUS	AX093197	396 bp	DNA	linear	PAT 30-MAR-2001
DEFINITION	AX093197	Sequence 15 from Patent WO0118046.		LOCUS	AX093197	396 bp	DNA	linear	PAT 30-MAR-2001
ACCESSION	AX093197	Sequence 15 from Patent WO0118046.		DEFINITION	AX093197	396 bp	DNA	linear	PAT 30-MAR-2001
VERSION	AX093197.1	GI:13509646		ACCESSION	AX093197	396 bp	DNA	linear	PAT 30-MAR-2001
KEYWORDS				VERSION	AX093197.1	GI:13509646			
SOURCE				KEYWORDS					
ORGANISM	human.			SOURCE					
REFERENCE	1 (bases 1 to 396)			ORGANISM	human.				
AUTHORS	Xu,J. and Stolck,J.A.			REFERENCE	1 (bases 1 to 396)				
TITLE	Ovarian tumor sequences and methods of use therefor			AUTHORS	Xu,J. and Stolck,J.A.				
JOURNAL	Patent: WO 0118046-A 15 15-MAR-2001;			TITLE	Ovarian tumor sequences and methods of use therefor				
FEATURES	Location/Qualifiers			JOURNAL	Patent: WO 0118046-A 15 15-MAR-2001;				
source	1..396			FEATURES	Location/Qualifiers				
misc_feature	1..396			source	1..396				
note	"n = A,T,C or G"			misc_feature	1..396				
BASE COUNT	129 a 83 c 121 g 62 t 1 others			note	"n = A,T,C or G"				

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcagcagagcttcacatc 21
 |||||||
 Db 79 CAGCAGCAGAGCTTCATCATC 59

RESULT 2
 HUMTRPM2A/c 1648 bp mRNA linear PRI 23-AUG-1996
 LOCUS Human TRPM-2 mRNA, complete cds.
 DEFINITION M64722
 ACCESSION M64722.1 GI:339972
 VERSION TRPM-2 protein.
 KEYWORDS Human cDNA to mRNA.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (sites)
 Wong, P., Talliefer, J., Lakin, J., Talliefer, D., Leger, J., Wang, C.
 and Tenniswood, M.
 Genomic organization and expression of the rat TRPM-2 (clusterin)
 gene, a gene implicated in apoptosis
 J. Biol. Chem. 268 (77), 5021-5031 (1993)
 93186813
 2 (bases 1 to 1648)
 Wong, P., Talliefer, D., Lakin, J., Pineault, J., Chader, G. and
 Tenniswood, M.
 Molecular characterization of human TRPM-2/clusterin, a gene
 associated with sperm maturation, apoptosis and neurodegeneration
 Eur. J. Biochem. 221 (3), 917-925 (1994)
 94237156

FEATURES

source
 1..1648
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

gene
 1..1648
 /gene="TRPM-2"

CDS
 53..1402
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 /protein_id="AAB06508.1"

translation="MMKTLLEFVGLLTWESGOVLGDTVSNDLEQNSKQYVVK
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 NETMALMECKPCKLQKOTCMKFAVAVCSGSLVROLEEFNOSPSPYFMWGDIDS
 SLENDROOHTMDVMODHFRASSTIDLEFDREPTREODTYHYLPSPHPRRPFR
 FPKSRIVRSFSPYEPPLNFMFQPEFLEIEAQAMDIFHSAPQHPTEPIRE
 EGDDRTVCREIRNSTGCLRMKQDCREILSDCSTNNPSQAKLREIDESLQVA
 ERLTRKYNELKSTQWKMNTSSLLEQLDEQFNWSRLANLTQGEDOYTLRVTVASH
 TSDSDVPSGVTVVVKLFDSDPITVTVPVEVSRKPKFMETVAEKALQEVKKHRE"

polyA_signal
 1627..1632
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BASE COUNT 408 a 488 c 440 g 312 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1648;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcagcagagcttcacatc 21
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 Db 73 CAGCAGCAGAGCTTCATCATC 53

RESULT 3
 A21577/c

LOCUS A21577 1651 bp DNA linear PAT 26-JUL-1994
 DEFINITION blood plasma component having a biological activity of inhibiting
 cytolysis mediated by a cytolytic protein.
 ACCESION A21577
 VERSION A21577.1 GI:579601
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1651)

REFERENCE
 AUTHORS Cytolysis INHIBITOR PROTEINS (CLI) AND DNA SEQUENCES CODING FOR
 SAID PROTEINS
 JOURNAL Patent: WO 9105043-A 3 18-Apr-1991;
 FEATURES Location/Qualifiers
 1..1651
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

CDS
 199..1545
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 activity of inhibiting cytolysis mediated by a cytolytic
 protein"
 /protein_id="CA01560.1"
 /db_xref="GI:579602"

translation="MMKTLLEFVGLLTWESGOVLGDTVSNDLEQNSKQYVVK
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 NETMALMECKPCKLQKOTCMKFAVAVCSGSLVROLEEFNOSPSPYFMWGDIDS
 SLENDROOHTMDVMODHFRASSTIDLEFDREPTREODTYHYLPSPHPRRPFR
 FPKSRIVRSFSPYEPPLNFMFQPEFLEIEAQAMDIFHSAPQHPTEPIRE
 EGDDRTVCREIRNSTGCLRMKQDCREILSDCSTNNPSQAKLREIDESLQVA
 ERLTRKYNELKSTQWKMNTSSLLEQLDEQFNWSRLANLTQGEDOYTLRVTVASH
 TSDSDVPSGVTVVVKLFDSDPITVTVPVEVSRKPKFMETVAEKALQEVKKHRE"

BASE COUNT 405 a 481 c 447 g 318 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 1651;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcagcagagcttcacatc 21
 |||||||
 Db 216 CAGCAGCAGAGCTTCATCATC 196

RESULT 4
 HUMCLI/c 1651 bp mRNA linear PRI 27-APR-1993
 LOCUS Human complement cytolysis inhibitor (CLI) mRNA, complete cds.
 DEFINITION M25915
 ACCESION M25915.1 GI:180619
 VERSION M25915.1
 KEYWORDS blood plasma glycoprotein; complement cytolysis inhibitor;
 secretory glycoprotein; seminal plasma protein; soluble terminal
 complement complex (C5b-9s) component.
 SOURCE Human (adult) liver, cDNA to mRNA, clone CLI-1.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1651)
 Jenne, D.E. and Tschopp, J.
 Molecular structure and functional characterization of a human
 complement cytolysis inhibitor found in blood and seminal plasma:
 identity to sulfated glycoprotein 2, a constituent of rat testis
 fluid
 Proc. Natl. Acad. Sci. U.S.A. 86, 7123-7127 (1989)
 89386692
 MEDLINE Draft entry and computer-readable sequence for [1] kindly submitted
 COMMENT by D.E.Jenne, 05-JUL-1989.
 FEATURES Location/Qualifiers
 1..1651

CDs
/organism="Homo sapiens"
/db_xref="taxon:9606"
199..1345
/note="complement cytolysis inhibitor precursor"
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/db_xref="GI:180620"

sig_peptide
/note="complement cytolysis inhibitor signal peptide"
mat_peptide
/product="complement cytolysis inhibitor a-chain"
mat_peptide
877..1342
/product="complement cytolysis inhibitor b-chain"
BASE COUNT 405 a 481 c 447 g 318 t
ORIGIN Unreported.

Query Match 100.0%; Score 21; DB 9; Length 1651;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcagcagagctctcatcat 21
|||||
DB 216 CAGCAGCAGAGCTCTCATCAT 196

RESULT 5
LOCUS BC019588/c 1658 bp mRNA linear PRI 22-JAN-2002
DEFINITION Homo sapiens, clusterin (complement lysis inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J), clone MGC:24903 IMAGE:4915444, mRNA, complete cds.

ACCESSION BC019588
VERSION BC019588.1 GI:18043614
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1658)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Strausberg, R.
JOURNAL Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnarone, P.H., Garcia, A.M., Lu, X., Huliy, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>
Series: IRAC Plate: 29 Row: m Column: 21

FEATURES
source
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502904.
Location/Qualifiers
1..1658

/organism="Homo sapiens"
/db_xref="LocusID:1191"
/db_xref="taxon:9606"
/clone="MGC:24903 IMAGE:4915444"
/tissue_type="Brain, anaplastic oligodendroglioma with 1p/19q loss"
/clone_11b="NCI-CGAP_Brn67"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"
49..1398

/codon_start=1
/product="clusterin (complement lysis inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)"
/protein_id="AAH19588.1"
/db_xref="GI:18043615"

/translation="MKTLLEFVGLLWESGOVLDQTVSDNELOEMSNQSKYVNE
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NEYMALMECKPCLOKCMKRYARVCRSGSLGRQLEELNOSPFYFMNGRID
SLENDROOTHMLDVMODHFRASSTIDELFQDRFTREPDYTHLYLPSLPKRPHE
FPKSRIVSLMPSPYEPPLNFAMQPELEMHQAQAMDHFHSPAFQHPPEFTRE
EGDDRTVCREIRHNSVGLRMKQDCRCREILSYDCSTNNPSQAKRLRELDSELOVA
ERTRKYNELKSYOKMKLNTSSLLEQNEQFNWVSRLANLTOGEOQYLRITYVASH
TSDDVSGVTEVYVKLFPSDPTITVTPVEVSRKPKFMETVAERKALOEYRKHRE"

BASE COUNT 423 a 486 c 439 g 310 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcagcagagctctcatcat 21
|||||
DB 69 CAGCAGCAGAGCTCTCATCAT 49

RESULT 6
LOCUS HSCSP40/c 1676 bp mRNA linear PRI 22-MAR-1995
DEFINITION Human SP-40, 40 mRNA for complement-associated protein SP-40, 40 alpha-1 and beta-1 chain.
X14723.1 GI:30250
KEYWORDS complement-associated protein; serum protein; SP-40, 40 gene.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1676)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Kirsbaum, L.
JOURNAL Direct Submission
Submitted (17-MAR-1989) Kirsbaum L., The University of Melbourne, The Preclinical Centre, School of Veterinary Science, Parkville Victoria 3052, Australia
2 (bases 1 to 1676)
Kirsbaum, L., Sharpe, J.A., Murphy, B., d'Aplice, A.J., Claesson, B., Hudson, P., and Walker, I.D.

Molecular cloning and characterization of the novel, human complement-associated protein, SP-40, 40: a link between the complement and reproductive systems
EMBO J. 8 (3), 711-718 (1989)
The sequence overlaps with that reported by Murphy et. al. in J. Clin. Invest. 81:1858-1864(1988).

FEATURES
source

1..1676
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/c1one="LK (107)"
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/c1one_ib="lambda g11"
48. .113
48. .1397
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/codon_start=1
/protein_id="CA32847.1"
/db_xref="GI:30251"
/db_xref="SWISS-PROT:P10909"
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NETMALMECKPCLKOTCMFYARVCSGSLGROLEEFINOSPFYWMGDRID
SLENDROOHTMDVMOHDFSRASSIIDLEFODPFRPODTHYLPFLPHRRHF
FPFKSRIVRELMFSPYEPUNHAFOPLEIHQAQOANDIHFSPAFOPHFERF
EGDDRTVCREIRHNSTGCLRMKDDCCKREILSYDCSTNNPSOAKLRRLDSLOYA
EILTRKYNELKSYOKMLNTSSLEQLEDFNNSRLANTGCEDDYLRRTTVASH
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114. .>114
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114. .1394
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729. .1394
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1622. .1627
/note="poc. polyA signal"
BASE COUNT      436 a      488 c      437 g      315 t
ORIGIN

Query Match      100.0%; Score 21; DB 9; Length 1676;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 cagcagcagagcttcacat 21
|||||
Db      68 CAGCAGCAGAGCTTCATCAT 48

RESULT 7
AX202086/c      1678 bp      DNA      linear      PAT 30-AUG-2001
LOCUS      AX202086
DEFINITION      Sequence 16 from Patent WO0153531.
ACCESSION      AX202086
VERSION      AX202086.1 GI:15391872
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 1678)
AUTHORS      Phippard,D., Vasanthakumari,G., Dotson,S. and Ma,X.J.
TITLE      Osteoarthritis tissue derived nucleic acids, polypeptides, vectors,
and cells
JOURNAL      Patent: WO 0153531-A 16 26-JUL-2001;
Pharmacia Corporation (US)
FEATURES
source      1. 1678
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      424 a      491 c      450 g      313 t
ORIGIN

Query Match      100.0%; Score 21; DB 6; Length 1678;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 cagcagcagagcttcacat 21
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Db      90 CAGCAGCAGAGCTTCATCAT 70

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```

RESULT 8
BC010514/c      1684 bp      mRNA      linear      PRI 12-JUL-2001
LOCUS      BC010514
DEFINITION      Homo sapiens, clusterin (complement lysis inhibitor, SP-40,40,
sulfated glycoprotein 2, testosterone-repressed prostate message 2,
apolipoprotein J), clone MGC:18080 IMAGE:4150452, mRNA, complete
cde
ACCESSION      BC010514
VERSION      BC010514.1 GI:14714740
KEYWORDS      MGC.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 1684)
AUTHORS      Strausberg,R
TITLE      Direct Submission
JOURNAL      Submitted (10-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc..
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalona@bcm.tmc.edu.
Villalona, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
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/db_xref="taxon:9606"
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/lab_host="DH10B"
/note="vector: pcMV-SPORT6"
69. .1418
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sulfated glycoprotein 2, testosterone-repressed prostate
message 2, apolipoprotein J)"
/protein_id="AAH0514.1"
/db_xref="GI:14714741"
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SLENDROOHTMDVMOHDFSRASSIIDLEFODPFRPODTHYLPFLPHRRHF
FPFKSRIVRELMFSPYEPUNHAFOPLEIHQAQOANDIHFSPAFOPHFERF
EGDDRTVCREIRHNSTGCLRMKDDCCKREILSYDCSTNNPSOAKLRRLDSLOYA
EILTRKYNELKSYOKMLNTSSLEQLEDFNNSRLANTGCEDDYLRRTTVASH
TSDSDVPSGYTEVYVKLEPDSPTITVTVPVEYSRKNPKFMETVAEKALQETRKHREE"
BASE COUNT      433 a      493 c      448 g      310 t
ORIGIN

Query Match      100.0%; Score 21; DB 9; Length 1684;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 cagcagcagagcttcacat 21

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Db 89 CAGCAGCAGAGCTTCATCAT 69

RESULT 9

LOCUS HUMTRPM2A1 7610 bp DNA linear PRI 23-AUG-1996

DEFINITION Human TRPM-2 protein gene, exons 1,2 and 3.

ACCESSION M63376

VERSION M63376.1 GI:292838

KEYWORDS TRPM-2 protein.

SEGMENT 1 of 4

SOURCE Human DNA.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (sites)

TITLE Wong,P., Pineault,J., Lakin,J., Taillefer,D., Leger,J., Wang,C. and Tenniswood,M.

JOURNAL gene, a gene implicated in apoptosis

MEDLINE J. Biol. Chem. 268 (7), 5021-5031 (1993)

REFERENCE 93186813

AUTHORS 2 (bases 1 to 7610)

TITLE Wong,P., Taillefer,D., Lakin,J., Pineault,J., Chader,G. and Tenniswood,M.

JOURNAL Molecular characterization of human TRPM-2/clusterin, a gene associated with sperm maturation, apoptosis and neurodegeneration

MEDLINE Eur. J. Biochem. 221 (3), 917-925 (1994)

FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

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/number=2

7021..7169

/gene="TRPM-2"

/number=3

BASE COUNT 1660 a 1994 c 2055 g 1899 t 2 others

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 7610;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagcttcacat 21

|||||

Db 5558 CAGCAGCAGAGCTTCATCAT 5538

RESULT 10

LOCUS AF235104/c 175382 bp DNA linear PRI 06-FEB-2002

DEFINITION Homo sapiens chromosome 8 clone GSI-251107 map 8p12, complete sequence.

ACCESSION AF235104

VERSION AF235104.3 GI:18543385

KEYWORDS HTG: HTGS_FULLTOP; HTGS_ACTIVEFIN.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 175382)

TITLE Wen,G., Reichwald,K., Baumgart,C., Taudin,S., Baumgart,C. and Platzer,M.

JOURNAL Chromosome 8 genomic sequence

ORIGIN

REFERENCE 2 (bases 1 to 175382)

AUTHORS Reichwald,K., Menzel,U., Dette,M., Baumgart,C., Jahn,N., Wen,G., Schillhabel,M. and Rosenthal,A.

JOURNAL Direct Submission

REFERENCE Submitted (16-FEB-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

AUTHORS 3 (bases 1 to 175382)

TITLE Genome Sequencing Center Jena.

JOURNAL Direct Submission

REFERENCE Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany

AUTHORS 4 (bases 1 to 175382)

TITLE Wen,G. and Platzer,M.

JOURNAL Direct Submission

REFERENCE Submitted (06-FEB-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT On Feb 6, 2002 this sequence version replaced gi:1852056.

----- Genome Center

Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: gscj-submit@genome.imb-jena.de

----- Project Information

Center project name: H342

Center clone name: GSI-251107

----- Summary Statistics

Sequencing vector: M13; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 172785 bases at least Q40

Consensus quality: 174289 bases at least Q30

Consensus quality: 174952 bases at least Q20

Quality coverage: 6.88 x in Q20 bases; sum-of-contigs

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality 10. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

FEATURES

source Location/Qualifiers

1..175382

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="8"

/map="8p12"

/clone="GSI-251107"

BASE COUNT 46563 a 38626 c 38604 g 51589 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 175382;

Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcagcagagcttcacat 21

|||||

Db 173418 CAGCAGCAGAGCTTCATCAT 173398

RESULT 11

LOCUS AC025192/c 187453 bp DNA linear HTG 13-MAY-2001

DEFINITION Homo sapiens chromosome 8 clone RP11-509E2 map 8, WORKING DRAFT

SEQUENCE, 7 unordered pieces.

ACCESSION AC025192

VERSION AC025192.3 GI:12313839

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORIGIN

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 187453)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 JOURNAL Homo sapiens chromosome 8, clone RP11-509E2
 REFERENCE 2 (bases 1 to 187453)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
 Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
 Campiano, A., Castle, A., Choquel, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hages, B., Heatford, A., Horton, L.,
 Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
 Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehocsky, J.,
 Levine, R., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R.,
 Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
 O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
 Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Teafaye, S., Theodore, J., Tirrell, A., Travers, M., Triggilio, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Jan 19, 2001 this sequence version replaced gi:6901239.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: MIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

 Project Information
 Center Project name: L5392
 Center Clone name: 509_E_2

 Summary Statistics
 Sequencing vector: M13; M7815; 48% of reads
 Sequencing vector: Plasmid; n/a; 52% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap, version 0.960731
 Consensus quality: 185120 bases at least Q40
 Consensus quality: 186074 bases at least Q30
 Consensus quality: 186533 bases at least Q20
 Insert size: 175000; agarose-fp
 Insert size: 186853; sum-of-contigs
 Quality coverage: 8.9 in Q20 bases; agarose-fp
 Quality coverage: 8.3 in Q20 ba.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 17773: contig of 17773 bp in length
 * 17774 17873: gap of 100 bp
 * 17874 20278: contig of 2405 bp in length
 * 20279 20378: gap of 100 bp
 * 20379 35742: contig of 15363 bp in length
 * 35743 35842: gap of 100 bp
 * 35843 65413: contig of 29571 bp in length
 * 65414 65513: gap of 100 bp
 * 65514 112793: contig of 47280 bp in length

FEATURES
 Source
 * 112794 112893: gap of 100 bp
 * 112894 150031: contig of 37138 bp in length
 * 150032 150131: gap of 100 bp
 * 150132 187453: contig of 37322 bp in length.
 Location/Qualifiers
 1..187453
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8"
 /clone="RP11-509E2"
 /clone_lib="RPC1-11 Human Male BAC"
 1..17773
 /note="assembly_fragment"
 /clone_end:SP6
 /vector_side:left
 17874..20278
 /note="assembly_fragment"
 /note="assembly_fragment"
 20379..35742
 /note="assembly_fragment"
 /note="assembly_fragment"
 35843..65413
 /note="assembly_fragment"
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 65514..112793
 /note="assembly_fragment"
 112894..150031
 /note="assembly_fragment"
 150132..187453
 /note="assembly_fragment"
 /clone_end:17
 /vector_side:right
 BASE COUNT 51878 a 43372 c 44058 g 47545 t 600 others
 ORIGIN
 Query Match 100.0%; Score 21; DB 2; length 187453;
 Best Local Similarity 100.0%; Pred. NO. 9.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 cagcagcagagctcctcatcat 21
 |||
 Db 124875 CAGCAGCAGAGCTCTCATCAT 124855

 RESULT 12
 AF311103/C 234431 bp DNA linear PRI 06-FEB-2002
 LOCUS
 DEFINITION Homo sapiens chromosome 8 clone scb-212e3 map 8p12, complete
 sequence.
 ACCESSION AF311103 GI:18542957
 VERSION
 KEYWORDS HTG; HTGS_FULTOP; HTGS_ACTIVEFIN.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 234431)
 AUTHORS Wen, G., Blechschmidt, K., Baumgart, C., Taudin, S., Baumgart, C. and
 Platzer, M.
 JOURNAL Chromosome 8 genomic sequence
 REFERENCE 2 (bases 1 to 234431)
 AUTHORS Blechschmidt, K., Jandrig, B., Baumgart, C., Dette, M.D., Jahn, N.,
 Menzel, U., Schillhabel, M.B., Wen, G., Taudien, S. and Rosenthal, A.
 TITLE Direct Submission
 JOURNAL Submitted (04-OCT-2000) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
 REFERENCE 3 (bases 1 to 234431)
 AUTHORS Wen, G. and Platzer, M.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-2002) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
 COMMENT On Feb 6, 2002 this sequence version replaced gi:14389409.

 Genome Center

Center: Institute of Molecular Biotechnology
 Center code: IMB
 Web site: <http://genome.imb-jena.de/>
 Contact: gscl-submit@genome.imb-jena.de
 ----- Project Information -----
 Center project name: H319
 Center clone name: SCB-212e3
 ----- Summary Statistics -----
 Sequencing vector: M13; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 233404 bases at least Q40
 Consensus quality: 234413 bases at least Q30
 Consensus quality: 234428 bases at least Q20
 Quality coverage: 5.81 x in Q20 bases; sum-of-coverage

----- Sequence Quality Assessment -----
 This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

FEATURES

Source
 1..234431
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8p12"
 /clone="SCB-212e3"
 BASE COUNT 62993 a 56257 c 55890 g 59291 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 234431;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cagcagcagagcttcctcatc 21
 ||||||||||||||||||||
 Db 13996 CAGCAGCAGAGCTTCATCAT 13976

RESULT 13
 DOGSP80/C 1636 bp mRNA linear MAM 27-Apr-1993
 DEFINITION DOG glycoprotein 80 (gp80) mRNA, complete cds.
 ACCESSION M55251.M38757
 VERSION M55251.1 GI:163953
 KEYWORDS glycoprotein 80.
 SOURCE Canis familiaris kidney cDNA to mRNA.
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 1636)
 Hartmann,K., Rauch,J., Urban,J., Parczyk,K., Diel,P., Pilarsky,C., Appel,D., Haase,W., Mann,K., Weller,A. and Koch-Brandt,C.
 Molecular cloning of gp 80, a glycoprotein complex secreted by kidney cells in vitro and in vivo: A link to the reproductive system and to the complement cascade
 J. Biol. Chem. 266, 9924-9931 (1991)
 JOURNAL MEDLINE 91236776
 FEATURES
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 1..1636
 /organism="Canis familiaris"
 /db_xref="taxon:9615"
 /cell_line="MDCK"
 /cell_type="epithelial-like"
 /tissue_type="kidney"
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gene

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 54..119
 /gene="gp80"
 /note="leader peptide"
 CDS
 54..1391
 /gene="gp80"
 /codon_start=1
 /evidence=experimental
 /product="glycoprotein 80"
 /protein_id="AAA30846.1"
 /db_xref="GI:163954"

misc_feature

120..732
 /gene="gp80"
 /note="p 35 subunit"

misc_feature

733..1388
 /gene="gp80"
 /note="p 45 subunit"

polyA_signal

1607..1612
 /gene="gp80"
 /note="potential; putative"

polyA_signal

1634..1636
 /gene="gp80"
 /note="potential; putative"

BASE COUNT 439 a 440 c 405 g 352 t
 ORIGIN

Query Match 92.4%; Score 19.4; DB 4; Length 1636;
 Best Local Similarity 95.2%; Pred. No. 64;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 cagcagcagagcttcctcatc 21
 ||||||||||||||||||||
 Db 74 CAGCAGCAGAGCTTCATCAT 54

RESULT 14
 AF118852/C 1678 bp mRNA linear MAM 19-NOV-2001
 DEFINITION Oryctolagus cuniculus apolipoprotein J/clusterin mRNA, complete cds.
 ACCESSION AF118852
 VERSION AF118852.1 GI:4580642
 KEYWORDS rabbit.
 SOURCE Oryctolagus cuniculus
 ORGANISM Oryctolagus cuniculus

REFERENCE 1 (bases 1 to 1678)
 Miyata,M., Biro,S., Kaieda,H., Eto,H., Orihara,K., Kihara,T., Obata,H., Matsushita,N., Matsuyama,T. and Tel.C.
 Apolipoprotein J/clusterin is induced in vascular smooth muscle cells after vascular injury
 Circulation 104 (12), 1407-1412 (2001)
 JOURNAL MEDLINE 21444720
 PUBMED 11560857

REFERENCE 2 (bases 1 to 1678)
 Miyata,M., Biro,S., Kaieda,H., Eto,H., Orihara,K., Kihara,T., Obata,H., Matsushita,N., Matsuyama,T. and Tel.C.
 Direct Submission
 Submitted (08-JAN-1999) First Department of Internal Medicine, Kagoshima University, 8-35-1 Sakuragaoka, Kagoshima 890-8520, Japan
 JOURNAL MEDLINE
 FEATURES
 Location/Qualifiers

source 1. .1678
/organism="Oryctolagus cuniculus"
/strain="Japanese white"
/db_xref="taxon:9986"
69.1412
/codon_start=1
/product="apolipoprotein J/clusterin"
/protein_id="A024461.1"
/db_xref="GI:4580643"
/translation="MTLLGCVGLLSMERGOVLGDOLVSPNLEOENSTOGSKYIDRE
IONAVGVOEIKTLIEKTEPERKTLISVLEAKKKKEDALNETRDSERKAKPEVGN
ETMALHEBCKPCLKQTCMKFYARICRSGSGVGLQLEPLNQSPTFYINCRIDS
LLENDROSHVDVWODSFNRATGIMDELFDQREFTTHPQDTFHSPTSTRPPLH
AKSRIVNIMPJLSLYGPLNFQDMFQPFEMIHQAQAMDVHLSPATQTPNVEITGG
PDDRACKEIRHNSTGCLRMKDOCAKCOEILSVDCSANNPSQNDLROELNDSLRAE
LTRRYNELLOSVMKMLNTSLLDQPNQEFNMVSQLANTLGTGPQDYLRVSTVSHTS
ESEAPSVFVYVVKLFPSDPTITFPEEVSRDNPFMETVAEKALOEYRKKRVE"

BASE COUNT 400 a 523 c 452 g 303 t

ORIGIN

Query Match 92.4%; Score 19.4; DB 4; Length 1678;
Best Local Similarity 95.2%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cagcagcagagtccttcacat 21
|||||

Db 86 CAGCAGCAGAGCTTCATCTT 66

RESULT 15
AF063235 3287 bp mRNA linear PLN 22-AUG-2000
LOCUS Pneumocystis carinii clone 15 variant 2 major surface glycoprotein
DEFINITION mRNA, complete cds.
ACCESSION AF063235
VERSION AF063235.1 GI:4321810
KEYWORDS
SOURCE
ORGANISM
Pneumocystis carinii.
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 3287)
Huang,S.N., Angus,C.W., Turner,R.E., Sorial,V. and Kovacs,J.A.
Identification and characterization of novel variant major surface
glycoprotein gene families in rat Pneumocystis carinii
J. Infect. Dis. 179 (1), 192-200 (1999)
99059868
9841839
2 (bases 1 to 3287)
Huang,S.N., Angus,C.W., Turner,R.E., Sorial,V. and Kovacs,J.A.
Direct Submission
Submitted (05-MAY-1998) Critical Care Medicine Department, Clinical
Center, National Institutes of Health, 9000 Rockville Pike,
Bethesda, MD 20892, USA
Location/Qualifiers
1..3287
/organism="Pneumocystis carinii"
/specific_host="rat"
/db_xref="taxon:4754"
/clone="15"
41..3175
/note="v2MSG"
/codon_start=1
/product="variant 2 major surface glycoprotein"
/protein_id="A015834.1"
/db_xref="GI:4321811"
/translation="MFSMINKIIVLILIVPIYGNQHLRVDRSPVSAENMLFE
DEVYKEDIYAILGDEYEVKSKSLAEYCNELKVIDPELKNVHTKVEICDNIE
OKGAGLNDKTEVEFSNPNRIYDALGNLKDQCKNNEKCIPLAEPRHDDPKENYK
LRRCYKIKROKAYADELLBALGKNKENDKCKEMETICPLTRESDEPMFSLNLT
KTCDDLSKLGSLVCLPKBELKDKDLKLEKCYERLEKCHFTGEACDADACQVFECKK
NNTYKAPESDFSPKPRASLTLMIGLEDVYNKAEKDGILIGKAGVDPRKLGITVFLQ

FEATURES
Source

CDS

DILLSDQVNMEDTVKRCNIMLERCNDLKHLENGEMTKLEEDGKRENNCKILLDVNVK
ERCTFRKSALEFQKDLSTOYNDDEKSELLPMGHLPTFTGECTELVSECFYLKNACTN
KIDACONVHACYKIKGRDLINKFPQKELRGKLGDRNSLSLKKCOEYVENCNTKL
DERYLPKCIYPRKCYVLSNIVVQSRELGVLIDGDRSLERKHLKEIGEKDELDRD
SNSNRKCATIKILCEYFVRAEKFRTYELKREDDAIDYQNTKALHEKCDTSLGEN
PFSISCALPRETCRYVYHTRDQRYLKDMMKNEGILEKTEDKKNANEITLVEELCT
TWGRHQVLVNCNDPDLGKERNGDQCEKLDKCRDPTKRLKSKDELTHLKGSLN
DKCRDALRKHCPDLQNGTFRILIDNCEMTVKELEKLVERYQNRCPYLKTDLEKAK
DELTEKDEYKAKOAEKSTEAARLLLSRONSSDSEOVSPLSAESSSSSELPP
PPPPONGPPTPDGASGTPGSGMPNYYKFGILVREYVAGVSEAEVAKAFDATYIALEL
YLELEKECKALELDGCFRDCPPNSKEVCGEIDTLCKEIEPLKDKPEKITEPCITLOT
TDIWTSTVSTVSTSTSMARCKPRTCTDSKERTQKQEBEVEYKPNQMKIRVPM
IKIMLGVTVGMG"

BASE COUNT 1277 a 407 c 731 g 872 t

ORIGIN

Query Match 87.6%; Score 18.4; DB 8; Length 3287;
Best Local Similarity 95.0%; Pred. No. 2e+02; Length 3287;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cagcagcagagtccttcacat 20
|||||

Db 2565 CAGCAGCAGAGTCATCATCA 2584

Search completed: May 17, 2002, 16:04:13
Job time: 16113 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 15:25:36 ; Search time 3628.41 Seconds
(without alignments)
78.116 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21
Sequence: 1 attgtctgagacgctcgtcgtc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	152	9	AM161759
2	21	100.0	156	9	BF922862
3	21	100.0	161	10	BF921576
4	21	100.0	165	10	BF92381
5	21	100.0	167	10	BF929953
6	21	100.0	169	10	BE766895
7	21	100.0	177	9	AL048592
8	21	100.0	177	10	BF958041
9	21	100.0	184	10	BF958930
10	21	100.0	185	10	BT036860
11	21	100.0	193	10	BT037432
12	21	100.0	193	10	BF944445
13	21	100.0	196	9	AT745406
14	21	100.0	201	10	BF957666
15	21	100.0	207	10	BF957858
16	21	100.0	218	9	AM807875
17	21	100.0	220	9	AT904991

18	21	100.0	223	10	BF920102	BF920102
19	21	100.0	224	9	AM161224	AM161224
20	21	100.0	226	10	BF935119	BF935119
21	21	100.0	227	10	BE841947	BE841947
22	21	100.0	229	10	BF950916	BF950916
23	21	100.0	236	9	AA339299	AA339299
24	21	100.0	238	10	BF921875	BF921875
25	21	100.0	243	10	BF923639	BF923639
26	21	100.0	243	10	AA336628	AA336628
27	21	100.0	244	10	BE766870	BE766870
28	21	100.0	248	10	BF923643	BF923643
29	21	100.0	252	10	BF923633	BF923633
30	21	100.0	253	10	BE887875	BE887875
31	21	100.0	253	10	BT041998	BT041998
32	21	100.0	256	10	BT041248	BT041248
33	21	100.0	257	9	AA365743	AA365743
34	21	100.0	262	10	BF947155	BF947155
35	21	100.0	266	9	AA352030	AA352030
36	21	100.0	268	10	BF920149	BF920149
37	21	100.0	272	10	BF956582	BF956582
38	21	100.0	273	10	BF956584	BF956584
39	21	100.0	274	10	BT036852	BT036852
40	21	100.0	277	9	AA351754	AA351754
41	21	100.0	280	10	BF935974	BF935974
42	21	100.0	283	10	BF947214	BF947214
43	21	100.0	284	10	BF959506	BF959506
44	21	100.0	293	9	AA318247	AA318247
45	21	100.0	294	9	AM498619	AM498619

ALIGNMENTS

RESULT 1
LOCUS AM161759
DEFINITION au70a10.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781594 3' similar to gb:xl4723 CLUSTERIN PRECURSOR (HUMAN);
mRNA sequence.
AM161759
AM161759.1 GI:6300792

ACCESSION AM161759 152 bp mRNA linear EST 09-NOV-1999
VERSION AM161759
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 152)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisell,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Merra,M., Martin,J., Moore,B., Schellenberg,K., Stepien,M., Tan,F., Thelsting,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Other ESTs: au70a10.y1

COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LINT; contact the
Image Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.

FEATURES

source
1..152
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2781594"
/clone_lib="Schneider fetal brain 00004"
/sex="male"
/tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"

/note="Organ: brain; Vector: pBluescript SK (Stratagene); Site_1: SctI; Site_2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-GAGAGAGAGAGAGAGCTCAAGATCTTAATTAAATTATCCCCCCCC-3' and 3' adaptor sequence: 5'-GAGAGAGAGAGCTGAGATTTTATTTTTTTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."

BASE COUNT 27 a 43 c 28 g 54 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 152;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 atgtctgagacgctcgtc 21
|||||
Db 100 ATTGCTGAGACGCTGCTC 120

RESULT 2
LOCUS BF922862 156 bp mRNA linear EST 19-JAN-2001
DEFINITION QV4-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF922862
VERSION BF922862.1 GI:12318659
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 156)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

FEATURES
SOURCE
1. 156
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="NT0247"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. letters patent application

No. 196/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 38 a 30 c 51 g 37 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 atgtctgagacgctcgtc 21
|||||
Db 94 ATTGCTGAGACGCTGCTC 74

RESULT 3
LOCUS BF921576 161 bp mRNA linear EST 19-JAN-2001
DEFINITION MR1-NT0179-171100-004-g01 NT0179 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF921576
VERSION BF921576.1 GI:12317464
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 161)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

FEATURES
SOURCE
1. 161
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="NT0179"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. letters patent application No. 196/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 44 a 29 c 53 g 35 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 161;
Best Local Similarity 100.0%; Pred. No. 4.5;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 attgtctgagaccgtctgctc 21
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Db 101 ATTGTCTGAGACCGCTCTGCTC 81

RESULT 4
BF929381 165 bp mRNA linear EST 19-JAN-2001
LOCUS IL2-NT0198-081200-280-G01 NT0198 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF929381
ACCESSION
VERSION BF929381.1 GI:12327509
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 165)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Ludwig Institute for Cancer Research
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2<2=IL2-NT0198-
081200-280-G01<3=2000-12-08<4=1)
Seq primer: puc 18 forward
High quality sequence stop: 165.
Location/Qualifiers
1..165
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0198"
/dev_stage="Adult"
/note="Organ: nervous.tumor; Vector: puc18; Site:1: Smat;
Site:2: Smat; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 27 a 47 c 31 g 60 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 attgtctgagaccgtctgctc 21
|||||

Db 112 ATTGTCTGAGACCGCTCTGCTC 132

RESULT 5
BF929953 167 bp mRNA linear EST 19-JAN-2001
LOCUS IL2-NT0198-111200-293-A03_1 NT0198 Homo sapiens cDNA, mRNA
DEFINITION

sequence.
BF929953
KEYWORDS BF929953.1 GI:12328185
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
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20202663
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2<2=IL2-NT0198-
111200-293-A03_1<3=2000-12-11<4=1)
Seq primer: puc 18 forward
High quality sequence stop: 165.
Location/Qualifiers
1..167
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0198"
/dev_stage="Adult"
/note="Organ: nervous.tumor; Vector: puc18; Site:1: Smat;
Site:2: Smat; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 60 a 32 c 48 g 27 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 attgtctgagaccgtctgctc 21
|||||

Db 54 ATTGTCTGAGACCGCTCTGCTC 34

RESULT 6
BE766895 169 bp mRNA linear EST 19-SEP-2000
LOCUS RC2-NT0110-050600-013-f03 NT0110 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE766895
ACCESSION BE766895
VERSION BE766895.1 GI:10196819
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 169)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

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20202663

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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6&2=RC2-NT0110-050600-013-f03&f3=2000-06-05&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 18

High quality sequence stop: 169.

FEATURES

source

1..169

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1lb="NT0110"

/dev_stage="Adult"

/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

37 a 36 c 37 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 21; DB 10; Length 169;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atgtctgagaccgtctgctc 21

|||||

Db- 125 ATTGCTGTGAGACCGTGTGTC 105

RESULT 7

AL048592/c 177 bp mRNA linear EST 01-MAR-2000

LOCUS

DEFINITION

DKFZP586H092.t1 586 (synonym: hute1) Homo sapiens cDNA clone

AL048592

AL048592.1 GI:4729143

EST.

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 177)

Pouscka, A., Kleih, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

EST (Pouscka, et al.)

Unpublished (1999)

Contact: Pouscka A.J.

Department Lehrbach

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Tel: +49-30-84131623

Fax: +49-30-84131128

Email: pouscka@mpg-berlin-dahlem.mpg.de

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ). Email: s.wiemann@dkfz-heidelberg.de; Sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZP586H092) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1..177

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="DKFZP586H092"

/clone_1lb="586 (synonym: hute1)"

/tissue_type="uterus"

/dev_stage="adult"

/lab_host="DH10B"

/note="Vector: pSPort1; Site_1: NotI; Site_2: SalI/MluI"

BASE COUNT

40 a 41 c 64 g 32 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 21; DB 9; Length 177;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atgtctgagaccgtctgctc 21

|||||

Db 143 ATTGCTGTGAGACCGTGTGTC 123

RESULT 8

BP958041 177 bp mRNA linear EST 22-JAN-2001

LOCUS

RC5-NN1165-281100-033-E03 NN1165 Homo sapiens cDNA, mRNA sequence.

DEFINITION

BP958041

BP958041.1 GI:12375316

EST.

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 177)

Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W., Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

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Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5&t2=RC5-NN1165-281100-033-E03&f3=2000-11-28&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 177.

FEATURES

source

1..177

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1lb="NN1165"

/dev.stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 63 a 34 c 52 g 28 t
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 atgtctgagaccgtctgctc 21
|||||
Db 68 ATTGCTGAGACCGCTCTGCTC 48

RESULT 9
BF958930/c 184 bp mRNA linear EST 22-JAN-2001
LOCUS PM1-NNI200-011200-009-g08 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF958930
ACCESSION BF958930
VERSION BF958930.1 GI:12376205
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 184)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NNI200-
01100-009-g08&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 184.

FEATURES

Source 1. 184
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="NNI200"
/dev.stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 47 a 36 c 61 g 40 t
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 atgtctgagaccgtctgctc 21
|||||
Db 108 ATTGCTGAGACCGCTCTGCTC 88

RESULT 10
BI036860/c 185 bp mRNA linear EST 14-JUN-2001
LOCUS MK4-NT0140-080101-209-c09 NT0140 Homo sapiens cDNA, mRNA sequence.
DEFINITION BI036860
ACCESSION BI036860
VERSION BI036860.1 GI:14443486
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 185)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MK4&t2=MK4-NT0140-
080101-209-c09&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 134.

FEATURES

Source 1. 185
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="NT0140"
/dev.stage="Adult"
/note="Organ: nervous tumor; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 41 a 42 c 62 g 40 t
ORIGIN

RESULT 11
 B1037432/c 190 bp mRNA linear EST 14-JUN-2001
 LOCUS B1037432
 DEFINITION CM3-NT0267-110101-588-h12 NT0267 Homo sapiens cDNA, mRNA sequence.
 ACCESSION B1037432
 VERSION B1037432.1 GI:144444058
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 190)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 2020263
 CONTACT: Simpson A.J.G.
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 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM3&t2=CM3-NT0267-
 110101-588-112&t3=2001-01-11&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 4
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="NT0267"
 /dev_stage="Adult"
 /note="Organ: nervous.tumor; Vector: puc18; Site.1: Sma1;
 Site.2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 76 a 38 c 49 g 27 t
 ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 190;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 attgtctgagacgctcgatc 21
 ||||||||||||||||||||
 Db 36 ATTGCTGAGACCGCTCGTC 16

RESULT 12
 BF944445/c 193 bp mRNA linear EST 22-JAN-2001
 LOCUS BF944445
 DEFINITION RC5-NN1165-131000-021-D04 NN1165 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF944445
 VERSION BF944445.1 GI:12361720
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc.Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 2020263
 CONTACT: Simpson A.J.G.
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 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5&t2=RC5-NN1165-
 131000-021-D04&t3=2000-10-13&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 193.
 Location/Qualifiers
 1. 193
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="NN1165"
 /dev_stage="Adult"
 /note="Organ: nervous.normal; Vector: puc18; Site.1: Sma1;
 Site.2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 70 a 39 c 57 g 27 t
 ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 193;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 attgtctgagacgctcgatc 21
 ||||||||||||||||||||
 Db 72 ATTGCTGAGACCGCTCGTC 52

RESULT 13
 A1745406 196 bp mRNA linear EST 17-DEC-1999
 LOCUS A1745406
 DEFINITION wc37d01.x1 NCI-CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2320801 3'
 similar to gb:x14723 CLUSTERTIN PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION A1745406
 VERSION A1745406.1 GI:5113694
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 196)
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/biopr/image/image.html
Insert length: 264 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES

source

Location/Qualifiers
1. 196
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2320801"
/clone_lib="NCI-CGAP_Pri28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI-CGAP_Pri22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 110192-1101959, and 121928-1220615)."
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

39 a 60 c 35 g 62 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 196;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 attgtctgagacgctctgctc 21
|||||
Db 101 attgtctgagacgctctgctc 121

RESULT 14
BF957666/c 201 bp mRNA linear EST 22-JAN-2001
LOCUS BF957666
DEFINITION PM1-NN1200-251100-007-c09 NN1200 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF957666
VERSION BF957666.1 GI:12374941
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 201)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

20020263
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL.
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t2=PM1-NN1200->

251100-007-c09&t3=2000-11-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 201.
Location/Qualifiers

FEATURES

source

1. 201
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1200"
/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18, Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT

52 a 39 c 71 g 39 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 attgtctgagacgctctgctc 21
|||||
Db 125 attgtctgagacgctctgctc 105

RESULT 15
BF957858/c 207 bp mRNA linear EST 22-JAN-2001
LOCUS BF957858
DEFINITION PM1-NN1200-271100-008-a07 NN1200 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF957858
VERSION BF957858.1 GI:12375133
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 207)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

20020263
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL.
([http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t2=PM1-NN1200-](http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t2=PM1-NN1200-271100-008-a07&t3=2000-11-27&t4=1)
271100-008-a07&t3=2000-11-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 182.
Location/Qualifiers

FEATURES

source

1. 207
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1200"
/dev_stage="Adult"

```

/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      51 a      45 c      71 g      40 t
ORIGIN

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Query Match      100.0%; Score 21; DB 10; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 attgctctgagacgctctgctc 21
        |||
Db      143 ATTGCTCTGAGACGCTCTGCTC 123

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Search completed: May 17, 2002, 15:25:38
Job time: 14515 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 17:58:43 ; Search time 147.64 Seconds
(without alignments)
66.563 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21

Sequence: 1 atgtctgagacgcgtctgtc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 424068 segs, 234053524 residues

Total number of hits satisfying chosen parameters: 848136

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	1614	US-10-119-428-31	Sequence 31, Appl
2	21	100.0	1839	US-60-365-384-115	Sequence 115, App
3	15.8	75.2	355	US-10-106-698-1758	Sequence 1758, App
4	15.2	72.4	200	US-09-539-331D-26988	Sequence 26988, A
5	15.2	72.4	251	US-09-975-254-18048	Sequence 18048, A
6	15	71.4	302	US-09-539-331D-33835	Sequence 33835, A
7	14.8	70.5	1482	US-10-103-627-30	Sequence 30, Appl
8	14.8	70.5	4109	US-09-741-148A-1	Sequence 1, Appl1
9	14.8	70.5	23668	US-09-741-148A-3	Sequence 3, Appl1
10	14.8	70.5	33958	US-10-105-299-14037	Sequence 14037, A
11	14.6	69.5	932	US-10-105-299-1118	Sequence 1118, App
12	14.6	69.5	1644	US-09-053-375B-823	Sequence 823, App
13	14.6	69.5	6162	US-10-105-299-12825	Sequence 12825, A
14	14.4	68.6	252	US-09-540-210B-2398	Sequence 2398, App
15	14.4	68.6	494	US-10-113-872-45	Sequence 45, Appl
16	14.4	68.6	518	US-09-539-331D-31816	Sequence 31816, A
17	14.4	68.6	1611	US-10-105-299-14778	Sequence 14778, A
18	14.4	68.6	1611	US-10-105-299-15187	Sequence 15187, A
19	14.2	67.6	331	US-09-673-476-310	Sequence 310, App
20	14.2	67.6	472	US-09-539-331D-33623	Sequence 33623, A
21	14.2	67.6	510	US-09-539-331D-34970	Sequence 34970, A
22	14.2	67.6	511	US-10-124-805-443	Sequence 443, App
23	14.2	67.6	614	US-10-105-299-11648	Sequence 11648, A
24	14.2	67.6	628	US-10-105-299-1905	Sequence 2095, App
25	14.2	67.6	648	US-09-930-213-190	Sequence 190, App
26	14.2	67.6	1326	US-09-749-728B-12	Sequence 12, Appl

27	14.2	67.6	1428	US-09-216-387-2	Sequence 2, Appl1
28	14.2	67.6	2177	US-09-722-377-4	Sequence 4, Appl1
29	14.2	67.6	2248	PCR-US02-09944-231	Sequence 231, App
30	14.2	67.6	2502	US-10-105-299-1215	Sequence 1215, App
31	14.2	67.6	2764	US-09-978-403A-258	Sequence 258, App
32	14.2	67.6	2764	US-09-978-544A-258	Sequence 258, App
33	14.2	67.6	2764	US-09-978-681A-258	Sequence 258, App
34	14.2	67.6	2764	US-09-978-757A-258	Sequence 258, App
35	14.2	67.6	2764	US-09-978-564A-258	Sequence 258, App
36	14.2	67.6	2764	US-09-999-831A-258	Sequence 258, App
37	14.2	67.6	2764	US-09-999-831A-258	Sequence 258, App
38	14.2	67.6	2764	US-09-978-375A-258	Sequence 258, App
39	14.2	67.6	2764	US-10-013-921A-258	Sequence 258, App
40	14.2	67.6	2764	US-10-013-921A-258	Sequence 258, App
41	14.2	67.6	2764	US-10-013-918A-258	Sequence 258, App
42	14.2	67.6	2764	US-10-017-082A-258	Sequence 258, App
43	14.2	67.6	2764	US-10-121-062-117	Sequence 117, App
44	14.2	67.6	4282	US-09-053-375B-1069	Sequence 1069, App
45	14.2	67.6	4997	US-10-105-299-9206	Sequence 9206, App

ALIGNMENTS

RESULT 1
US-10-119-428-31/c
Sequence 31, Application US/10119428
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Wehrman, Tom
APPLICANT: Ren, Feiyan
APPLICANT: Ma, Yundang
APPLICANT: Zhou, Ping
APPLICANT: Zhao, Qing A.
APPLICANT: Dmanac, Radolje T.
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 789CIP2
CURRENT APPLICATION NUMBER: US/10/119,428
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PL_FL_genes Version 1.0
SEQ ID NO 31
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (116)..(1465)
US-10-119-428-31

Query Match 100.0%; Score 21; DB 6; Length 1614;
Best local Similarity 100.0%; Pred. No. 0.06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtctgagacgcgtctgtc 21
Db 202 ATGTCTGAGACGCCTGTGTC 182

RESULT 2
US-60-365-384-115/c

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Sequence 115, Application US/60365384
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Zhiwei
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Ghosh, Malabika
APPLICANT: Zhao, Qing A.
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyun
APPLICANT: Xue, Aidong J.
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Gezhi
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 814 Polypeptides
CURRENT APPLICATION NUMBER: US/60/365,384
CURRENT FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 666
SOFTWARE: pc_FL_genes Version 6.0
SEQ ID NO 115
LENGTH: 1839
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (132)..(1316)
US-60-365-384-115

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Query Match	100.0%	Score 21	DB 7	Length 1839
Best Local Similarity	100.0%	Pred. No.	0.061	
Matches	21	Conservative	0	Mismatches 0; Indels 0; Gaps 0
Qy	1 attgctctgagaccgtctgctc	21		
Db	218 attgctctgagaccgtctgctc	198		

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RESULT 3
US-10-106-698-1758/c
; Sequence 1758, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; * TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA00551
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 1758
; LENGTH: 355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc-feature
; LOCATION: (353)..(353)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc-feature
; LOCATION: (355)..(355)
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OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1758

Query Match	75.28;	Score 15.8;	DB 6;	Length 355;
Best Local Similarity	89.58;	Pred. NO. 30;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

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QY      3  tgtctgagaccgctctgtc 21
          |||||
Db      308 TGTCTGAGTCCCTCTGCTC 290
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```

RESULT 4
US-09-539-331D-26988/c
; Sequence 26988, Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mollahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 26988
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00420089
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 106
; OTHER INFORMATION: a, t, c, g, or other
US-09-539-331D-26988

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```

Query Match          72.4%; Score 15.2; DB 5; Length 200;
Best Local Similarity 85.0%; Pred. No.59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2  ttgtctgagaccgtctgctc 21
          |||||  || |||||  ||
Db      26  ttgtctgacacctgtctgctc 7

RESULT 5
US-09-975-254-18048/c
; Sequence 18048, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 18048
; LENGTH: 251
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700955068H1

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US-09-975-254-18048

Query Match 72.4%: Score 15.2; DB 5; Length 251;
Best Local Similarity 85.0%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ttgtctgagacgctcgtg 21
||||| ||||| |||||
DB 226 TTGTCTGAGACCCACTGTGTC 207

RESULT 6
US-09-539-331D-33835/c
Sequence 33835, Application US/09339331D

GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleage, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
FILE REFERENCE: PD-1022 CIP
CURRENT APPLICATION NUMBER: US/09/539,331D
CURRENT FILING DATE: 2000-03-30
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 40961
SOFTWARE: PERL Program
SEQ ID NO 33835
LENGTH: 302
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu01211390
US-09-539-331D-33835

Query Match 71.4%: Score 15; DB 5; Length 302;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 tctgagacgctcgtg 19
||||| ||||| |||||
DB 284 TCTGAGACCGCTGCG 270

RESULT 7
US-10-102-627-30/c
Sequence 30, Application US/10102627

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PR24CI
CURRENT APPLICATION NUMBER: US/10/102,627
CURRENT FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 110
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 1482
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1453)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc.feature
LOCATION: (1474)
OTHER INFORMATION: n equals a,t,g, or c
US-10-102-627-30

Query Match 70.5%: Score 14.8; DB 6; Length 1482;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ttgtctgagacgctcgtg 19
||||| ||||| |||||
DB 439 TTGTCTGAGACCATATGCG 422

RESULT 8
US-09-741-148A-1/c
Sequence 1, Application US/09741148A

GENERAL INFORMATION:
APPLICANT: Chunhua YAN et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CLO00566
CURRENT APPLICATION NUMBER: US/09/741,148A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/206,982
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4109
TYPE: DNA
ORGANISM: Homo sapien
US-09-741-148A-1

Query Match 70.5%: Score 14.8; DB 5; Length 4109;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 gctctgagacgctcgtg 21
||||| ||||| |||||
DB 1127 GTCTGAGACAGCTTGTGTC 1110

RESULT 9
US-09-741-148A-3/c
Sequence 3, Application US/09741148A

GENERAL INFORMATION:
APPLICANT: Chunhua YAN et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CLO00566
CURRENT APPLICATION NUMBER: US/09/741,148A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/206,982
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 23668
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(23668)
OTHER INFORMATION: n = A,T,C or G
US-09-741-148A-3

Query Match 70.5%: Score 14.8; DB 5; Length 23668;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 gctctgagacgctcgtg 21
||||| ||||| |||||

PRIOR APPLICATION NUMBER: 60/014,010
PRIOR FILING DATE: March 25, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/903,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: 60/030,144
PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996
PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998
PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751

PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 2398
LENGTH: 252
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu00275763
NAME/KEY: unsure
LOCATION: 198, 249
OTHER INFORMATION: a, t, c, g, or other
US-09-540-2108-2398

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Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 15
US-10-113-872-45
Sequence 45, Application US/10113872
GENERAL INFORMATION:
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 494
TYPE: DNA
ORGANISM: Homo sapiens
US-10-113-872-45

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Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 tgcctgagacgctg 18
Db 273 tgcctgagacgctg 288

Search completed: May 17, 2002, 17:58:45
Job time: 9179 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 17:56:00 ; Search time 5965.48 Seconds
(without alignments)
76.160 Million cell updates/sec

Title: US-09-913-325-5
Perfect score: 21
Sequence: 1 atgtctgagaccgtctgctc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues
Total number of hits satisfying chosen parameters: 43959072

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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ALIGNMENTS

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; Sequence 5, Application PC/TUS0004875
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: ANTISENSE THERAPY FOR CANCER
; FILE REFERENCE: UBC.P-020-WO
; CURRENT APPLICATION NUMBER: PCT/US00/04875
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121,726
; EARLIER FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
PCT-US00-04875-5

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; Sequence 5, Application US/09913325
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-WO
; CURRENT APPLICATION NUMBER: US/09/913,325
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
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; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-913-325-5
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 5, Application US/09944326
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-5
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; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
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LENGTH: 21
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; ORGANISM: HUMAN
; FEATURE:
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US-10-080-794-5
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Best Local Similarity 100.0%; Pred. No. 2.1;
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; Sequence 4414, Application US/09716472
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2033-001
; CURRENT APPLICATION NUMBER: US/09/716,472
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/166,601
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 6233
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4414
; LENGTH: 168
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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US-09-716-472-4414
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; Sequence 10776, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLECULES
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10776
; LENGTH: 173
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01344983
US-09-534-840-10776
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Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 77 ATTGCTGAGACCGCTCTGCTC 57
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; Sequence 10325, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLECULES
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
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; LENGTH: 177
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01113942
US-09-534-840-10325
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Query Match          100.0%; Score 21; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 attgtctgagaccgtctgctc 21
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Db 154 ATTGCTGAGACCGCTCTGCTC 134
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RESULT 8
US-09-534-840-10415/c
; Sequence 10415, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLECULES
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10415
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu01055183
NAME/KEY: unsure
LOCATION: 17, 40
OTHER INFORMATION: a, t, c, g, or other
US-09-534-840-10415

Query Match 100.0%; Score 21; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attgtctgagaccgtctgtgc 21
|||||
Db 154 ATTGCTGAGACCGTCTGTGTC 134

RESULT 9

US-09-534-840-10784/c
Sequence 10784, Application US/09534840
GENERAL INFORMATION:
APPLICANT: Sellhammer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullaly, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLEC
FILE REFERENCE: PD-1010 CIP
CURRENT APPLICATION NUMBER: US/09/534,840
CURRENT FILING DATE: 1992-07-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 13675
SOFTWARE: PERL Program
SEQ ID NO 10784
LENGTH: 190
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu01342214
US-09-534-840-10784

Query Match 100.0%; Score 21; DB 20; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attgtctgagaccgtctgtgc 21
|||||
Db 154 ATTGCTGAGACCGTCTGTGTC 134

RESULT 10

US-09-534-840-10412/c
Sequence 10412, Application US/09534840
GENERAL INFORMATION:
APPLICANT: Sellhammer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullaly, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLEC
FILE REFERENCE: PD-1010 CIP
CURRENT APPLICATION NUMBER: US/09/534,840
CURRENT FILING DATE: 1992-07-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 13675
SOFTWARE: PERL Program
SEQ ID NO 10412
LENGTH: 192
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu01085063
NAME/KEY: unsure
LOCATION: 119, 124, 134, 175
OTHER INFORMATION: a, t, c, g, or other
US-09-534-840-10412

Query Match 100.0%; Score 21; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attgtctgagaccgtctgtgc 21
|||||
Db 76 ATTGCTGAGACCGTCTGTGTC 56

RESULT 11

US-08-485-657-14/c
Sequence 14, Application US/08485657
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/199,900
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-485-657-14

Query Match 100.0%; Score 21; DB 8; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attgtctgagaccgtctgtgc 21
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Db 153 ATTGCTGAGACCGTCTGTGTC 133

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RESULT 12
US-09-366-380-14/C
; Sequence 14, Application US/09366380
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-366-380-14

Query Match          100.0%; Score 21; DB 17; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 attgtctgagaccgtctgctg 21
   |||||||||||||||||||
DB 153 ATTGCTGAGACCGCTGCTGTC 133

RESULT 13
US-09-534-840-9752/C
; Sequence 9752, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLE
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
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; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 9752
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01227727
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-534-840-9752

Query Match          100.0%; Score 21; DB 20; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 attgtctgagaccgtctgctg 21
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DB 153 ATTGCTGAGACCGCTGCTGTC 133

RESULT 14
US-09-534-840-10336/C
; Sequence 10336, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MO
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10336
; LENGTH: 203
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01308898
US-09-534-840-10336

Query Match          100.0%; Score 21; DB 20; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 attgtctgagaccgtctgctg 21
   |||||||||||||||||||
DB 154 ATTGCTGAGACCGCTGCTGTC 134

RESULT 15
US-09-534-840-9756/C
; Sequence 9756, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MO
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
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; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 9756
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu01099825
US-09-534-840-9756

Query Match 100.0%; Score 21; DB 20; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 attgtctgagacgctcgtc 21
|||||
Db 136 ATGCTGTGAGACGCTGTGTC 116

Search completed: May 17, 2002, 17:56:00
Job time: 12667 sec

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OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:06:10 ; Search time 111.1 Seconds
(Without alignments)
46.429 Million cell updates/sec

Title: US-09-913-325-5

Sequence: 1 atgtctgagacgctctgtc 21

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Gapop 10.0 , Gapext 1.0 .

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	100.0	195	2	US-08-485-657A-14
C 2	21	100.0	195	5	PCR-US95-02303-14
C 3	19.4	92.4	181	2	US-08-485-657A-19
C 4	19.4	92.4	181	5	PCR-US95-02303-18
C 5	15.2	72.4	6671	1	US-08-280-443-1
C 6	15.2	72.4	6671	1	US-08-457-459-1
C 7	15.2	72.4	6671	1	US-08-555-678-1
C 8	15.2	72.4	6671	5	PCR-US95-02275-1
C 9	15.2	72.4	6671	1	US-08-151-574-31
C 10	15.2	72.4	6671	2	US-08-419-448-31
C 11	15.2	72.4	6671	2	US-08-233-510-31
C 12	14.8	70.5	1438	3	US-09-187-331-4
C 13	14.8	70.5	1438	4	US-09-470-946-4
C 14	14.8	70.5	3563	4	US-09-041-886-20
C 15	14.8	70.5	3596	2	US-08-779-801-5
C 16	14.8	70.5	3596	4	US-09-298-441-5
C 17	14.6	69.5	2820	5	PCR-US93-11725-1
C 18	14.6	69.5	2820	1	US-08-015-985-4
C 19	14.4	68.6	2002	2	US-08-715-202A-3
C 20	14.2	67.6	331	4	US-09-060-756-310
C 21	14.2	67.6	939	4	US-09-105-390-45
C 22	14.2	67.6	944	2	US-08-522-421-2
C 23	14.2	67.6	1020	4	US-09-105-390-61
C 24	14.2	67.6	1130	1	US-07-864-004B-1
C 25	14.2	67.6	1130	1	US-08-251-937A-1
C 26	14.2	67.6	1130	1	US-08-212-133A-5
C 27	14.2	67.6	1130	1	US-08-474-503-3

C 28	14.2	67.6	1130	2	US-08-670-707A-3	Sequence 3, Appl
C 29	14.2	67.6	1130	4	US-09-037-601-3	Sequence 3, Appl
C 30	14.2	67.6	1130	5	PCR-US93-03275-1	Sequence 1, Appl
C 31	14.2	67.6	1130	5	PCR-US94-13200-3	Sequence 1, Appl
C 32	14.2	67.6	1428	2	US-08-786-999-2	Sequence 2, Appl
C 33	14.2	67.6	1428	4	US-08-969-987-8	Sequence 8, Appl
C 34	14.2	67.6	1494	1	US-08-585-758A-3	Sequence 3, Appl
C 35	14.2	67.6	1494	1	US-08-977-818-3	Sequence 3, Appl
C 36	14.2	67.6	1494	2	US-08-670-274B-3	Sequence 3, Appl
C 37	14.2	67.6	1494	2	US-09-146-187-3	Sequence 3, Appl
C 38	14.2	67.6	1623	1	US-08-121-202-3	Sequence 3, Appl
C 39	14.2	67.6	2200	1	US-08-592-126-102	Sequence 102, App
C 40	14.2	67.6	2512	4	US-09-105-390-7	Sequence 7, Appl
C 41	14.2	67.6	4334	2	US-08-670-707A-38	Sequence 38, Appl
C 42	14.2	67.6	4334	4	US-09-037-601-38	Sequence 38, Appl
C 43	14.2	67.6	6402	2	US-08-670-707A-36	Sequence 36, Appl
C 44	14.2	67.6	6402	4	US-09-037-601-36	Sequence 36, Appl
C 45	14.2	67.6	7032	4	US-09-324-867-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-485-657A-14/c
Sequence 14, Application US/08485657A
Patent No. 5942389
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-485-657A-14

Query Match 100.0%; Score 21; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgtctgagacgctctgtc 21


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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,443
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6671 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 155..3832
US-08-280-443-1

Query Match      72.4% Score 15.2; DB 1; Length 6671;
Best Local Similarity 85.0%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 ttgtctgagaccgtctgtgc 21
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DB      808 TTGGCTATGACCGTCTGTGTC 789

RESULT      6
US-08-457-459-1/c
Sequence 1, Application US/08457459
Patent No. 5677428
GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,459
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49CUSA
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6671 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 155..3832
US-08-457-459-1
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Query Match      72.4% Score 15.2; DB 1; Length 6671;
Best Local Similarity 85.0%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 ttgtctgagaccgtctgtgc 21
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DB      808 TTGGCTATGACCGTCTGTGTC 789
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RESULT      7
US-08-555-678-1/c
Sequence 1, Application US/08555678
Patent No. 5763174
GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,678
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49DUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6671 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: Lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253
; FEATURE:
; NAME/KEY: Intron
; LOCATION: 254..355
; FEATURE:
; NAME/KEY: exon
; LOCATION: 356..1715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(210..253, 356..1715)
; OTHER INFORMATION: /codon_start=210
; OTHER INFORMATION: /product="Phytase"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 210..380
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 381..1712
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function="inositol phosphate
; OTHER INFORMATION: /phosphatase"
; OTHER INFORMATION: /product="Phytase"
; OTHER INFORMATION: /evidence=EXPERIMENTAL
;
US-09-233-510-31

Query Match 72.4%; Score 15.2; DB 4; Length 6756;
Best Local Similarity 85.0%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ttgtctgagaccgtctgtc 21
DB 130 TTATATGAGACCGTCGGGTC 149

RESULT 12
US-09-187-331-4/C
; Sequence 4, Application US/09187331
; Patent No. 6043056
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina A.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS
; FILE REFERENCE: PF-0631 US
; CURRENT APPLICATION NUMBER: US/09/187,331
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1438
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```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2705267
;
US-09-187-331-4

Query Match 70.5%; Score 14.8; DB 3; Length 1438;
Best Local Similarity 88.9%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 gctctgagaccgtctgtc 21
DB 1232 GTCGTGAGACATCTGTCTC 1215

RESULT 13
US-09-470-946-4/C
; Sequence 4, Application US/09470946
; Patent No. 6358923
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina A.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS
; FILE REFERENCE: PF-0631 US
; CURRENT APPLICATION NUMBER: US/09/470,946
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: US 09/187,331
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2705267
;
US-09-470-946-4

Query Match 70.5%; Score 14.8; DB 4; Length 1438;
Best Local Similarity 88.9%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 gctctgagaccgtctgtc 21
DB 1232 GTCGTGAGACATCTGTCTC 1215

RESULT 14
US-09-041-886-20/C
; Sequence 20, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabinzaden, Shantoz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 3563 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 3..3550
US-09-041-886-20

Query Match          70.5%; Score 14.8; DB 4; Length 3563;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 tgctgagacgctcgt 20
   |||||  |||||
Db 2385 TGCTGAGATGCTCTGCT 2368

RESULT 15
US-08-779-801-5/c
Sequence 5, Application US/08779801
Patent No. 5853995
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of
TITLE OF INVENTION: Diseases and a Diagnostic Test for Spinocerebellar Ataxia Type
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,801
FILING DATE: January 7, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3596
TYPE: nucleic acid

```

```

STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cDNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: brain
IMMEDIATE SOURCE:
LIBRARY: Primary human brain cDNA
CLONE: BI-1(V2)-GGCAG
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 19p13
US-08-779-801-5

Query Match          70.5%; Score 14.8; DB 2; Length 3596;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 tgctgagacgctcgt 20
   |||||  |||||
Db 2385 TGCTGAGATGCTCTGCT 2368

Search completed: May 17, 2002, 16:06:12
Job time: 12746 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:13:54 ; Search time 447.74 Seconds
(without alignments)
80.527 Million cell updates/sec

Title: US-09-913-325-5
Sequence: 1 attgtctgagaccgtctgtc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

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4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

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13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

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21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	21	21	AAA94227	Human testosteorone
2	100.0	195	16	AAT00416	Genetic suppressor
3	100.0	396	22	AAF94824	Human ovarian cancr
4	100.0	491	21	AAO3751	Human secreted pro
5	100.0	512	20	AAV89150	EST Clone CGI. Ho
6	100.0	572	20	AAZ42136	Human normal blad
7	100.0	922	21	AAA43857	Human secreted exp
8	100.0	1568	22	AA544948	CDNA encoding nove
9	100.0	1651	12	AAO11503	Cytolysis Inhibito

C	10	21	100.0	1678	22	AAH23086	Osteoarthritis tis
C	11	17.8	84.8	518	22	AAD05495	Human secreted pro
C	12	17.8	84.8	518	22	AAD05522	Human secreted pro
C	13	17.8	84.8	1670	22	AAD08210	Human secreted pro
C	14	17.8	84.8	1670	22	AAD05523	Human secreted pro
C	15	17.8	84.8	1670	22	AAD08191	Human secreted pro
C	16	16.2	77.1	2304	22	AA545136	CDNA encoding nove
C	17	16.2	77.1	325791	22	AA543104	Human Oestrogen re
C	18	16	76.2	11674	22	AAK70965	Human Immune/haema
C	19	15.8	75.2	355	22	AAH34666	Human colon cancer
C	20	15.8	75.2	1580	22	AA530562	DNA encoding novel
C	21	15.8	75.2	1580	22	AAO66165	Human reproductive
C	22	15.8	75.2	8888	20	AAK02665	BP-892047, Seg ID 4
C	23	15.4	73.3	374	22	AA532978	DNA encoding CAR1
C	24	15.4	73.3	2097	23	ABL05375	Drosophila melanog
C	25	15.4	73.3	4284	23	ABL05374	Drosophila melanog
C	26	15.4	73.3	6245	23	ABL19688	Drosophila melanog
C	27	15.4	73.3	6632	23	ABL19686	Drosophila melanog
C	28	15.4	73.3	6655	23	ABL05612	Drosophila melanog
C	29	15.2	72.4	51	22	AAH79918	Human DNA containi
C	30	15.2	72.4	332	22	AAO1942	Human reproductive
C	31	15.2	72.4	342	22	ABA71312	Human foetal liver
C	32	15.2	72.4	342	22	AAK19616	Human brain expres
C	33	15.2	72.4	342	22	AAK45622	Human bone marrow
C	34	15.2	72.4	342	22	AAI51555	Probe #20241 used
C	35	15.2	72.4	366	21	AAO48862	Arabidopsis thalia
C	36	15.2	72.4	367	21	AAO34794	Human foetal liver
C	37	15.2	72.4	484	22	AA585877	Human brain expres
C	38	15.2	72.4	484	22	AAK06899	Human bone marrow
C	39	15.2	72.4	484	22	AAK32397	Probe #6926 used t
C	40	15.2	72.4	484	22	AAI38240	DNA encoding novel
C	41	15.2	72.4	579	23	AA565858	DNA encoding novel
C	42	15.2	72.4	1466	23	AA580037	DNA encoding novel
C	43	15.2	72.4	1668	23	AA592996	DNA encoding novel
C	44	15.2	72.4	1668	23	AA593802	DNA encoding novel
C	45	15.2	72.4	1803	22	AAO05175	Human secreted pro

ALIGNMENTS

RESULT 1	AAA94227	standard; DNA; 21 BP.
ID	AAA94227	
XX	AAA94227:	
AC	12-JAN-2001 (first entry)	
XX		
DT		
XX		
DE	Human testosteorone-repressed prostate message-2 antisense oligo #3.	
XX		
KW	Human: testosteorone-repressed prostate message-2; TRPM-2; clusterin; sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200049937-A2.	
XX		
PD	31-AUG-2000.	
XX		
PF	25-FEB-2000; 2000WO-US04875.	
XX		
PR	26-FEB-1999; 99US-0121726.	
XX		
PA	(UYBR-) UNIV BRITISH COLUMBIA.	
PI	Cleave M, Rennie PS, Miyake H, Nelson C;	
XX	WPI: 2000-533132/48.	
DR		
XX		
PT	Treating prostatic tumors and renal cancers by antisense inhibition of the testosteorone-repressed prostate messenger-2 gene -	
XX		

PS Claim 4: Page 36: 38pp: English.
XX
CC The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clustel1n, suitel1n, glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed
CC at human TRPM-2 can be used in the treatment of tumour cells expressing
CC the TRPM-2 gene. These include prostate cancer, renal cell cancer and
CC some breast cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective.
XX
SQ Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 other:

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attgctgagaccgtctgctgc 21
Db 1 attgctgagaccgtctgctgc 21

RESULT 2
AAf00416/c
ID AAT00416 standard; CDNA; 195 BP.
XX
AC AAT00416;
XX
DT 26-MAR-1996 (first entry)
XX
DE Genetic suppressor element HL7.1.
XX
KM Genetic suppressor element; GSE; platinum-based drug; cisplatin;
KM chemotherapy; HL7.1; testosterone-repressed prostatic message-2; TRPM-2;
KM ss.
XX
OS Synthetic.
XX
PN WO9522612-A2.
XX
PD 24-AUG-1995.
XX
PF 22-FEB-1995; 95WO-US02303.
XX
PR 22-FEB-1994; 94US-0199900.
XX
PA (UNIT I) UNIV ILLINOIS FOUND.
XX
PI Gudkov A, Kirschling DJ, Roninson IB;
XX
DR WPI: 1995-302718/39.
XX
PT Genetic suppressor elements which confer resistance to
PT platinum-based drugs, eg. cisplatin, on cancer cells - useful for
PT enhancement of chemotherapy, and for diagnosis of resistance to
PT these drugs.
XX
PS Claim 14; Fig 17: 75pp: English.
XX
CC The sequences represented by AAT00405-T00418 are genetic suppressor
CC elements (GSEs). This sequence represents GSE HL6.10. This sequence
CC shows homology to the CDNA encoding testosterone-repressed prostatic
CC message-2 (TRPM-2). These sequences were obtained from a cDNA library
CC derived from the total CDNA of a cisplatin sensitive cell. Genetic
CC suppressor elements confer resistance to platinum-based drugs (PDS),
CC such as cisplatin. These functional GSEs can then be used to create
CC probes for the parent gene. The probes can then be used in a method of
CC measuring the level of GSE gene expression. The GSEs can be used in
CC methods of diagnosis of resistance to PDS by measuring the level of
CC expression of GSE genes. The GSEs are also used in methods to overcome
CC resistance to PDS in cancer cells. The GSEs (or fragments of them) can

CC be used to inhibit the function of genes associated with sensitivity to
CC PDS. For enhancement of chemotherapy, a GSE can be transferred (either
CC alone or with another gene) on an expression vector into blood
CC progenitor cells from a cancer patient. The cells are returned to the
CC patient's circulation and allowed to repopulate the blood before
CC aggressive chemotherapy is carried out (using higher cisplatin
CC concentrations than normal), this will thereby avoid toxic side effects
CC to the immune system as the blood cells will be GSE resistant.
XX
SQ Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 other:

Query Match 100.0%; Score 21; DB 16; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attgctgagaccgtctgctgc 21
Db 153 ATTGCTGAGACCGTCTGCTC 133

RESULT 3
AAf94824/c
ID AAF94824 standard; CDNA; 396 BP.
XX
AC AAF94824;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human ovarian cancer associated coding sequence SEQ ID NO: 15.
XX
KM Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200118046-A2.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-US24827.
XX
PR 10-SEP-1999; 99US-0394374.
PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA;
XX
DR WPI: 2001-211395/21.
XX
PT Isolated polypeptides associated with ovarian carcinomas, and the
PT nucleic acids that encode them, useful for the prevention diagnosis and
PT treatment of ovarian cancers -
XX
PS Claim 18; Page 120: 189pp: English.
XX
CC The present invention provides a number of coding sequences and proteins,
CC the over-expression of which is associated with ovarian carcinoma/cancer.
CC These can be used in the diagnosis, treatment and prevention of ovarian
CC cancer, optionally by gene therapy or in the form of a vaccine. The
CC present sequence is an example of one of these sequences.
XX
SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other:

Query Match 100.0%; Score 21; DB 22; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attgctgagaccgtctgctgc 21
XXXXXXXXXXXXXXXXXXXXXXXXXXXX

Db 145 ATTGCTGAGACCGTCTGCTC 125

RESULT 4

AAC03751/c
ID AAC03751 standard; cDNA: 491 BP.

XX AAC03751;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 3749.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

PN EPI033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PA (GEST) GENSET.

PI Dumas Mline Edwards J, Duclert A, Giordano J;

DR WPI: 2000-500381/45.

XX P-PSDB: AAC03745.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
diagnosing CDNA and genomic DNAs that correspond to 5' ESTs and for
diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX Claim 1: SEQ ID 3749; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
CDNA encoding secreted proteins. An ORF has been identified within the
sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
derived from 30 different tissues. EST sequences usually correspond
mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
well suited for isolating cDNA sequences derived from the 5' ends of
CDNA and even in those cases where longer cDNA sequences have been
obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CDNA with intact 5' ends and can therefore be used to obtain full length
CDNA and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
vectors.

XX Sequence 491 BP; 149 A; 114 C; 149 G; 78 T; 1 other;

Query Match 100.0%; Score 21; DB 21; Length 491;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 1 atgtctgagaccgtctgctc 21

DB 194 ATTGCTGAGACCGTCTGCTC 174

RESULT 5

AAV89150/c
ID AAV89150 standard; cDNA: 512 BP.

XX AAV89150;

DT 15-FEB-1999 (first entry)

XX EST clone CGL.

DE

KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
KW gene therapy; ss.

XX Homo sapiens.

PN W09845436-A2.

PD 15-OCT-1998.

PF 10-APR-1998; 98WO-US06955.

PR 10-APR-1997; 97US-0838821.

PA (GENETICS INST INC.

PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;

PR Racine LA, Spaulding V, Treacy M;

DR WPI: 1999-070077/06.

PT New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
ovary, pituitary, retina and colon cDNA libraries.

XX Claim 1: Page 126; 618pp; English.

XX The present sequence represents a human expressed sequence tag (EST).
CC The polynucleotide, which is a secreted EST, and the encoded protein
are predicted to have useful biological activities which would make
them suitable for treating, preventing or ameliorating medical
conditions in humans and animals, although no supporting data is
CC given. Suggested activities include nutritional activity, immune
stimulating or suppressing activity, haematopoiesis regulating
activity, tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
activity, receptor/ligand activity, anti-inflammatory activity,
cadherin/tumour invasion suppressor activity, tumour inhibition
activity. The polynucleotide may also be useful for gene therapy.

XX Sequence 512 BP; 154 A; 114 C; 150 G; 94 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 512;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 1 atgtctgagaccgtctgctc 21

DB 121 ATTGCTGAGACCGTCTGCTC 101

AA42136/c
ID AA42136 standard; cDNA: 572 BP.

XX AA42136;

DT 31-JAN-2000 (first entry)

DE Human normal bladder tissue cDNA derived EST 15.

KW Human; bladder; treatment; EST; expressed sequence tag; cytostatic;
KW cancer; gene therapy; ss.

XX Homo sapiens.

PN DE19818620-A1.

```

PD 28-OCT-1999.
XX
XX 21-APR-1998; 98DE-1018620.
XX
XX 21-APR-1998; 98DE-1018620.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pflarsky C, Dahl E;
XX WPI: 1999-602416/52.
XX
XX New polypeptides and their nucleic acids, useful for treatment of
XX bladder tumour and identification of therapeutic agents -
XX
XX Claim 3; Page 158; 366pp; German.
XX
XX This invention describes novel polypeptide fragment sequences (I) and
XX their encoding nucleic acids (II) which are highly expressed in normal
XX bladder tissue and have cytostatic activity. (II) are used for
XX recombinant expression of (I) and to isolate complete genes. (I) are
XX used to identify agents suitable for the treatment of bladder tumours,
XX to directly treat this form of cancer (including expression from gene
XX therapy vectors), or are used in a preparation for cancer treatment. (I)
XX is also used for the generation of specific antibodies. (II) are
XX identified by assembling ESTs (expressed sequence tags) from a
XX particular tissue type before comparison of expression patterns. This
XX allows a significantly longer fragment of the gene to be revealed, and
XX therefore reduces the number of failures because of ESTs from different
XX libraries representing different parts of the same unknown gene
XX distorting the estimated frequency of occurrence in a particular tissue.
XX AA42122-242248 represent EST fragments derived from a human normal
XX bladder tissue cDNA library which encode the protein fragments
XX represented in AAY60329-Y60591.
XX
XX Sequence 572 BP; 161 A; 128 C; 186 G; 97 T; 0 other:
SQ
Query Match 100.0%; Score 21; DB 20; Length 572;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 attgctgagacgctctgctc 21
DB 262 ATTGCTGTGAGACCGCTGTGCTC 242

```

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XX
XX WO200021991-A1.
XX
XX 20-APR-2000.
XX
XX 15-OCT-1999; 99WO-US24206.
XX
XX 15-OCT-1998; 98US-0104436.
XX
XX (GENY ) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M, Bowman MR;
XX WPI: 2000-317938/27.
XX
XX Isolated polynucleotides, and encoded proteins, comprising secreted
XX expressed sequence tags (SESTs), useful for treating various disorders
XX such as autoimmune, infectious, and central nervous system disorders -
XX
XX Claim 1; Page 316; 803pp; English.
XX
XX AAA43426 to AAA45925 represent specifically claimed secreted expressed
XX sequence tags (SESTs), isolated from human, mouse, chicken and rat
XX tissue sources. The SESTs can have a range of activities depending on
XX the tissues they were isolated from. The activities include:
XX chemotactic; proliferative; immunomodulatory; haematopoietic;
XX cyostatic; analgesic; haemostatic; thrombolytic; antiinflammatory;
XX antihistaminic; antibacterial; antifungal; antiviral; antidiabetic;
XX neurotropic; antiparkinsonian; antipsoriatic; cerebroprotective;
XX anticonvulsant; and antidepressant. The SESTs can be used for gene
XX therapy and in vaccines. The SESTs are useful as probes for the
XX identification and isolation of full-length cDNAs and genomic DNA
XX molecules which correspond to the SESTs. Proteins encoded by the SESTs
XX are useful in assays for determining biological activity and raising
XX antibodies. They may be useful for treatment of autoimmune disorders
XX (multiple sclerosis, insulin dependent diabetes), allergic conditions
XX (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
XX osteoporosis, osteoarthritis, central nervous system disorders
XX (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
XX disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
XX disease), tumours, bacterial, fungal or viral infections, depression and
XX psoriasis. AAA45926 to AAA45931 represent linker variants which are given
XX in the exemplification of the present invention.
XX
XX Sequence 922 BP; 243 A; 265 C; 244 G; 166 T; 4 other:
SQ
Query Match 100.0%; Score 21; DB 21; Length 922;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 attgctgagacgctctgctc 21
DB 118 ATTGCTGTGAGACCGCTGTGCTC 98

```

```

RESULT 7
AAA43857/C
ID AAA43857 standard; cDNA; 922 BP.
XX
AC AAA43857;
XX
XX 21-AUG-2000 (first entry)
XX
DE Human secreted expressed sequence tag SEQ ID NO:432.
XX
XX Human: mouse; chicken; rat; secreted expressed sequence tag; SEST;
XX expressed sequence tag; EST; probe; chemotactic; proliferative;
XX immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
XX thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
XX antiviral; antidiabetic; antihistaminic; vulnary; antiparkinsonian;
XX antitumor; osteoprotective; neuroprotective; neurotropic; antipsoriatic;
XX cerebroprotective; anticonvulsant; antidepressant; gene therapy;
XX vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
XX insulin dependent diabetes; asthma; osteoporosis; osteoarthritis;
XX lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
XX central nervous system disorder; Alzheimer's disease; stroke;
XX Parkinson's disease; Huntington's disease; coagulation disorder;
XX haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
XX tumour; infection; depression; psoriasis; ss.
XX
XX Homo sapiens.
OS

```


KM gut protection; lung; liver fibrosis; immune deficiency; infection;
 KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KM fertility; analgesic; pain; antigen; ss.
 OS Homo sapiens.
 PN W0200166689-A2.
 XX
 XX
 PD 13-SEP-2001.
 PE
 XX 05-MAR-2001; 2001WO-US04942.
 XX
 XX 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665353.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 DR WPI: 2001-589934/66.
 DR P-PSDB: AAU28048.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Claim 1; SEQ ID No 29; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.
 CC
 XX
 SQ Sequence 1568 BP; 386 A; 456 G; 434 C; 292 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 1568;
 Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 atgtctgagacgctctgctc 21
 ||||||||||||||||
 Db 156 ATTGCTGTGAGACCGCTCTGCTC 136

RESULT 9
 AAQ11503/C
 ID AAQ11503 standard; DNA; 1651 BP.
 XX
 AC AAQ11503:
 XX
 DT 20-JUN-1991 (first entry)
 XX
 XX Cytolysis Inhibitor gene.
 DE Cytolysis Inhibitor gene.
 XX
 KM Cytolysis inhibitor; perforin; immunological effector molecule;
 KM fertility; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH sig_peptide 199..261
 FT /*tag= a
 FT mat_peptide 262..1542
 FT /*tag= b
 FT /product= cytolysis inhibitor
 XX
 PN DE3933850-A.
 XX
 PD 18-APR-1991.
 XX
 PF 06-OCT-1989; 89DE-3933850.
 XX
 PR 06-OCT-1989; 89DE-3933850.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Tschopp J, Jenne D;
 XX
 DR WPI: 1991-118338/17.
 XX
 XX DNA sequence coding for cytolysis inhibitor - is strong inhibitor
 PT of terminal complement protein, e.g. perforin secreted by killer
 PT cells
 XX
 PS Claim 2; Page 8; 15pp; German.
 XX
 CC Two probes were prepared based on the known partial amino acid
 CC sequences of both chains of the Cytolysis inhibitor and used to
 CC screen a liver-specific cDNA library. One clone which hybridised
 CC positively to both probes was found to contain a 1.7kb BamHI-KpnI
 CC fragment. This was inserted into plasmid pGEM4, to give pGEM4/Z1-1.
 CC E.coli transformed with the plasmid are deposited under DSM # 5269.
 CC The insert has the sequence given in this file.
 CC
 XX
 SQ Sequence 1651 BP; 405 A; 481 C; 447 G; 318 T; 0 other;

Query Match 100.0%; Score 21; DB 12; Length 1651;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 atgtctgagacgctctgctc 21
 ||||||||||||||||
 Db 282 ATTGCTGTGAGACCGCTCTGCTC 262

RESULT 10
 AAH23086/C
 ID AAH23086 standard; DNA; 1678 BP.

[illegible]

KW	inflammation; neurological disorder; Alzheimer's disease; food additive;
KV	angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
KM	pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW	cell culture; chemotaxis; vulnerability; binding partner identification;
KW	gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	81..419
FT	/tag- a
FT	/product= "Human secreted protein precursor"
FT	/transl_except= (pos:367..369, aa:Xaa)
FT	/transl_except= (pos:414..416, aa:Xaa)
FT	/note= "Xaa corresponds to any of the naturally occurring
FT	L-amino acids"
FT	sig_peptide
FT	81..143
FT	/tag- b
FT	mat_peptide
FT	144..416
FT	/tag- c
FT	/product= "Mature human secreted protein"
PN	WO200134767-A2.
XX	
PD	17-MAY-2001.
XX	
PF	01-NOV-2000; 2000MO-US30036.
XX	
PR	05-NOV-1999; 99US-0163576.
PR	27-JUL-2000; 2000US-0221366.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	Soppet DR, Komatsoulis G, Shi Y, Olsen HS, Ruben SM;
XX	
DR	WPI: 2001-316492/73.
DR	P-PSDB: AAE01675.
PT	Isolated nucleic acid molecule encoding a human secreted protein 1s
XX	used in preventing, treating or ameliorating a medical condition -
XX	
Claim 1:	Page 413; 540pp; English.
CC	AAD05492-AA05564 represent cDNAs corresponding to 22 human secreted
CC	protein genes, and AAEO1672-AAEO1743 represent the proteins they encode.
CC	AAO01744-AAO01763 represent human secreted protein fragments or variants.
CC	The secreted proteins and their genes are useful for preventing, treating
CC	or ameliorating medical conditions, e.g., by protein or gene therapy.
CC	Pathological conditions can be diagnosed by determining the amount of the
CC	new protein in a sample or by determining the presence of mutations in
CC	the new genes. Specific uses are described for each of the 22 genes,
CC	based on the tissues in which they are most highly expressed, and include
CC	developing products for the diagnosis or treatment of proliferative
CC	disorders, cancer, tumours, foetal and developmental abnormalities,
CC	hematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC	diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC	neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC	cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC	psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC	angiodysplasia-related disorders, kidney disorders, gastrointestinal disorders,
CC	pregnancy-related disorders, endocrine disorders, and infections. The
CC	proteins can also be used to aid wound healing and epithelial cell
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs
CC	before transplantation, for supporting cell culture of primary tissues,
CC	to regenerate tissues, to identify their cognate ligands or binding
CC	partners, and in chemotaxis, and can be used as a food additive or
CC	preservative to modify storage properties. Antibodies specific for a
CC	protein of the invention can be used in alleviating symptoms associated
CC	with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC	radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC	The present sequence represents a human secreted protein-encoding cDNA of
XX	the invention.

SQ Sequence 518 BP; 146 A; 123 C; 148 G; 96 T; 5 other:

Query Match 84.8%; Score 17.8; DB 22; Length 518;
Best Local Similarity 90.5%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atgtctgagaccgtctgctc 21
1 |||||
Db 164 AGTGTCTGAGACCATCTGCTC 144

RESULT 12
AAD05522/c
ID AAD05522 standard; cDNA: 518 BP.

AC AAD05522;
XX
XX 18-JUL-2001 (first entry)

DE Human secreted protein-encoding gene 4 cDNA clone HOF0C33, SEQ ID NO:41.
XX
XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KM foetal abnormality; developmental abnormality; haematopoietic disorder;
KM immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KM Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KM psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KM inflammation; neurological disorder; Alzheimer's disease; food additive;
KM angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;
KM pregnancy-related disorder; endocrine disorder; infection; wound healing;
KM cell culture; chemotaxis; vulnery; binding partner identification;
XX gene therapy; ss.
OS Homo sapiens.
XX

FT Key Location/Qualifiers
FH 81..419
FT /tag= a
FT /product= "Human secreted protein precursor"
FT /transl_except= (pos:291..293, aa:xaa)
FT /transl_except= (pos:387..389, aa:xaa)
FT /transl_except= (pos:414..416, aa:xaa)
FT /note= "Xaa corresponds to any of the naturally occurring
FT l-amino acids"
FT 81..131
FT /tag= b
FT 132..416
FT /tag= c
FT /product= "Mature human secreted protein"

XX
PN W0200134767-A2.
XX
XX 17-MAY-2001.
XX
XX 01-NOV-2000; 2000MO-US30036.
XX
XX 05-NOV-1999; 99US-0163576.
PR 27-JUL-2000; 2000US-0221366.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
XX
XX Sopet DR, Komatsoulis G, Shi Y, Olsen HS, Ruben SM;
PI WPI: 2001-316492/33.
XX
XX P-PSDB; AAE01702.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 1; Page 434; 540p; English.
XX
XX AAD05492-AAD05564 represent cDNAs corresponding to 22 human secreted
CC protein genes, and AAE01672-AAE01743 represent the proteins they encode.

CC AAE01744-AAE01763 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 22 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein-encoding cDNA of
CC the invention.
XX

SQ Sequence 518 BP; 146 A; 122 C; 148 G; 95 T; 7 other:

Query Match 84.8%; Score 17.8; DB 22; Length 518;
Best Local Similarity 90.5%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atgtctgagaccgtctgctc 21
1 |||||
Db 164 AGTGTCTGAGACCATCTGCTC 144

RESULT 13
AAD08210/c
ID AAD08210 standard; cDNA: 1670 BP.

AC AAD08210;
XX
XX 07-AUG-2001 (first entry)

DE Human secreted protein-encoding gene 1 cDNA clone HOF0C33, SEQ ID NO:30.
XX
XX Human; secreted protein; proliferative disorder; cancer; tumour;
KM foetal abnormality; developmental abnormality; haematopoietic disorder;
KM immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KM inflammation; allergy; neurological disorder; Alzheimer's disease;
KM Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KM skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KM cardiovascular disorder; angiogenic disorder; kidney disorder;
KM gastrointestinal disorder; pregnancy-related disorder;
KM endocrine disorder; infection; wound healing; vulnery;
KM cell culture; chemotaxis; food additive; gene therapy;
KM binding partner identification; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 76..495
FT CDS
FT /tag= a
FT /product= "Human secreted protein precursor"
FT /transl_except= (pos:126
FT 76..126
FT /tag= b
FT 127..492
FT /tag= c
FT /product= "Mature human secreted protein"

XX WO200132837-A1.
 PN 10-MAY-2001.
 XX
 XX 17-OCT-2000; 2000WO-US28664.
 PF
 XX 02-NOV-1999; 99US-0163085.
 XX 17-DEC-1999; 99US-0172411.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Fiscella M, Wei P, Lafleur DW, Olsen HS, Baker K, Ebner R,
 PI Komatsoulis G, Rosen CA, Ruben SM, Duan RD, Young PE, Florence KA;
 PI Moore PA, Birse CE, NI J, Soppet DR, Shi Y;
 XX WPI: 2001-328782/34.
 DR P-PSDB; AAE03783.
 XX
 PT Novel human secreted proteins and nucleic acids for diagnosing,
 PT preventing and treating neurological, cardiovascular, infectious,
 PT autoimmune, gastrointestinal, bone disorders, cancer, particularly
 PT ovarian cancer.
 XX
 PS Claim 1; Page 384-385; 421pp; English.
 XX
 CC AAD08191-AAD08213 represent cDNAs corresponding to 19 human secreted
 CC protein genes, and AAE03764-AAE03786 represent the proteins they encode.
 CC AAE03787-AAE03800 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 19 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein-encoding cDNA of the invention.
 XX
 SQ Sequence 1670 BP; 425 A; 473 C; 436 G; 336 T; 0 other;

Query Match 84.88; Score 17.8; DB 22; Length 1670;
 Best Local Similarity 90.58; Pred. NO. 15;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

0y 1 attgtctgagaccgtctgtgc 21
 1 |||||
 DB 159 AGTGTCTGAGACCACTGCTC 139

RESULT 14
 AAD05523/c
 ID AAD05523 standard; CDNA: 1670 BP.
 XX
 AC AAD05523;

XX 18-JUL-2001 (first entry)
 DT
 XX
 DE Human secreted protein-encoding gene 4 cDNA clone HOF0C33, SEQ ID NO:42.
 XX
 XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
 KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;
 KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
 KW cell culture; chemotaxis; vulnerability; binding partner identification;
 KW gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 XX Key Location/Qualifiers
 FH 76..495
 FT CDS /*tag= a
 FT /*product= "Human secreted protein precursor"
 FT sig_peptide 76..126
 FT /*tag= b
 FT mat_peptide 127..492
 FT /*tag= c
 FT /*product= "Mature human secreted protein"
 XX
 XX WO200134767-A2.
 PN 17-MAY-2001.
 XX
 XX 01-NOV-2000; 2000WO-US30036.
 PD
 XX
 XX 05-NOV-1999; 99US-0163576.
 PF
 XX 27-JUL-2000; 2000US-0221366.
 PR
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Soppet DR, Komatsoulis G, Shi Y, Olsen HS, Ruben SM;
 PI WPI: 2001-316492/33.
 DR P-PSDB; AAE01703.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 PS Claim 1; Page 434-435; 540pp; English.
 XX
 CC AAD05492-AAD05564 represent cDNAs corresponding to 22 human secreted
 CC protein genes, and AAE01742-AAE01763 represent the proteins they encode.
 CC AAE01744-AAE01763 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing, treating
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 22 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumours, foetal and developmental abnormalities,
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a

CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein-encoding cDNA of
CC the invention.

XX Sequence 1670 BP; 425 A; 473 C; 435 G; 336 T; 0 other;

Query Match 84.8%; Score 17.8; DB 22; Length 1670;
Best Local Similarity 90.5%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;
OY 1 attgtctgagacgctgctgc 21
DB 159 AGTGTCTGAGACCATCTGCTC 139

RESULT 15
AAD08191/c
ID AAD08191 standard; cDNA; 1684 BP.

AC AAD08191;
DT 07-AUG-2001 (first entry)

XX Human secreted protein-encoding gene 1 cDNA clone HOF0C33, SEQ ID NO:11.
DE
XX
XX Human secreted protein; proliferative disorder; cancer; tumour;
KM foetal abnormality; developmental abnormality; haematopoietic disorder;
KM immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KM inflammation; allergy; neurological disorder; Alzheimer's disease;
KM Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KM skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KM cardiovascular disorder; angiogenic disorder; kidney disorder;
KM gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KM endocrine disorder; infection; wound healing; vulnery;
KM cell culture; chemotaxis; food additive;
KM binding partner identification; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 91..1182
FT /*tag= a
FT sig_peptide /product= "Human secreted protein precursor"
FT /*tag= b
FT mat_peptide 154..1179
FT /*tag= c
FT /product= "Mature human secreted protein precursor"

PN WO200132837-A1.

XX 10-MAY-2001.

XX 17-OCT-2000; 2000MO-US28664.

XX 02-NOV-1999; 99US-0163085.

XX 17-DEC-1999; 99US-0172411.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Fisceila M, Wei P, Lafleur DW, Olsen HS, Baker K, Ebner R;

XX Komatsoulis G, Rosen CA, Ruben SM, Duan RD, Young PE, Florence KA;

XX Moore PA, Birse CE, Ni J, Soppet DR, Shi Y;

XX WPI; 2001-328782/34.

XX P-PSDB; AAE03764.

PT Novel human secreted proteins and nucleic acids for diagnosing,
PT preventing and treating neurological, cardiovascular, infectious,
PT autoimmune, gastrointestinal, bone disorders, cancer, particularly

PT ovarian cancer -
XX
XX Claim 1; Page 375; 421pp; English.

CC AAD08191-AAD08213 represent cDNAs corresponding to 19 human secreted
CC protein genes and AAE03764-AAE03787 represent the proteins they encode.
CC AAE03787-AAE03800 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 19 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunoassay (ELISA). The present sequence represents a human
CC secreted protein-encoding cDNA of the invention.

XX Sequence 1684 BP; 429 A; 478 C; 435 G; 342 T; 0 other;

Query Match 84.8%; Score 17.8; DB 22; Length 1684;
Best Local Similarity 90.5%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;
OY 1 attgtctgagacgctgctgc 21
DB 174 AGTGTCTGAGACCATCTGCTC 154

Search completed: May 17, 2002, 16:13:55
Job time: 7047 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:04:13 ; Search time 1959.41 Seconds
(without alignments)
224.280 Million cell updates/sec

Title: US-09-913-325-5

Sequence: 1 atgtctgagacgctgtgtc 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb_da: 2: gb_htg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vi: 15: em_da: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vi: 30: em_htg_hum: 31: em_htg_inv: 32: em_htg_other: 33: em_htgo_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	21	100.0	396	6	AX093197	AX093197 Sequence
2	21	100.0	1648	9	HUMTRPM2A	M64722 Human TRPM-
3	21	100.0	1651	6	A21577	A21577 blood plasm
4	21	100.0	1651	9	HUMCL1	M25915 Human compl
5	21	100.0	1658	9	BC019588	BC019588 Homo sapi
6	21	100.0	1676	9	HSCSP40	X14723 Human SP-40
7	21	100.0	1678	6	AX202086	AX202086 Sequence
8	21	100.0	1684	9	BC010514	BC010514 Homo sapi
9	21	100.0	7610	9	HUMTRPM2A1	M63376 Human TRPM-
10	21	100.0	175382	2	AF235104	AF235104 Homo sapi
11	21	100.0	187453	2	AC025192	AC025192 Homo sapi
12	21	100.0	224431	9	AF311103	AF311103 Homo sapi
13	17.8	84.8	136131	9	AC000360	AC000360 Homo sapi
14	17.8	84.8	171830	2	AC092103	AC092103 Homo sapi
15	17.8	84.8	173513	9	HS125H2	Z98949 Human DNA s
16	17.8	84.8	191410	10	AC083814	AC083814 Mus muscu
17	17.8	84.8	227872	2	AC020786	AC020786 Mus muscu
18	17.8	84.8	288888	9	HSJ1069C8	AJ110932 Homo sapi
19	17.4	82.9	177102	9	AT062323	AT062323 Homo sapi
20	16.8	80.0	345	9	SCM1	AY062323 Homo sapi
21	16.8	80.0	43961	1	AL445986	AL445986 Human DNA
22	16.8	80.0	120873	9	AP004762	AP004762 Oryza sat
23	16.8	80.0	138036	2	AC012243	AC012243 Homo sapi
24	16.8	80.0	144136	2	AC093648	AC093648 Homo sapi
25	16.8	80.0	161547	2	AC069422	AC069422 Homo sapi
26	16.8	80.0	163240	2	AC015765	AC015765 Homo sapi
27	16.8	80.0	165570	2	AC002460	AC002460 Human BAC
28	16.8	80.0	174952	9	AP004620	AP004620 Oryza sat
29	16.8	80.0	177664	2	AC079507	AC079507 Mus muscu
30	16.8	80.0	179262	2	AC064812	AC064812 Mus muscu
31	16.8	80.0	180793	2	AC100112	AC100112 Mus muscu
32	16.4	78.1	58431	2	AC095616	AC095616 Rattus no
33	16.4	78.1	58431	2	AC099305	AC099305 Rattus no
34	16.4	78.1	79726	2	AC096975	AC096975 Rattus no
35	16.4	78.1	91953	2	AX315020	AX315020 Sequence
36	16.4	78.1	215164	2	G50193	G50193 SHG-79716
37	16.2	77.1	264	6	AK058077	AK058077 Homo sapi
38	16.2	77.1	418	11	AF118852	AF118852 Oryctolag
39	16.2	77.1	1502	9	BC007910	BC007910 Homo sapi
40	16.2	77.1	1678	4	AF370145	AF370145 Arabidopsi
41	16.2	77.1	1704	9	AE007202	AE007202 Sinornitho
42	16.2	77.1	1874	8	AE009113	AE009113 Agrobacte
43	16.2	77.1	2290	8		
44	16.2	77.1	10381	1		
45	16.2	77.1	11557	1		

ALIGNMENTS

RESULT 1
LOCUS AX093197/c 396 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 15 from Patent WO0118046.
ACCESSION AX093197
VERSION AX093197.1 GI:13509646

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source
1.396
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature
1.396
/note="n = A,T,C or G"
BASE COUNT 129 a 83 c 121 g 62 t 1 others

CDS

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IONAVNGKQIKTLIEKTEERKTLISLEAKKKEDALNETRESETKLELPGVCN
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LLENDROQTHMDVMDHFSRASSIIIDELFODRFTREPQDTYHYLPFSLPHRPHF
FPKSRIVSRSLMPEFSEYELNFMHAFQPELEMIHBAQOAMDIHFSPAFQHPFEIR
GGDDRTVCREIRHNSTGCLRKMDCCDKREILSVDCSTNNPSQAKLRRELDSELOVE
RLTRKYNELKSYOKMKMLNTSLLLEOLNEOPNMYSRLANLTGEGDYLYLEVTYASH
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262..876
/product="complement cytolysis inhibitor a-chain"
mat_peptide
877..1542
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BASE COUNT
405 a 481 c 447 g 318 t
ORIGIN
Unreported.
Query Match
Best Local Similarity 100.0%; Score 21; DB 9; Length 1651;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgtctgagaccgtctgctc 21
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Db 282 ATTGCTGAGACCGTCTGCTC 262
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RESULT 5
LOCUS BC019588 1658 bp mRNA linear PRI 22-JAN-2002
DEFINITION Homo sapiens, clusterin (complement lysis inhibitor, SP-40, 40,
sulfated glycoprotein 2, testosterone-repressed prostate message 2,
apolipoprotein J), clone MGC:24903 IMAGE:4915444, mRNA, complete
cds.
ACCESSION BC019588
VERSION BC019588.1 GI:18043614
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1658)
Strausberg, R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnathure, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 29 Row: m Column: 21

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FEATURES

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/db_xref="locusid:1191"

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1p/19q 10s"

/clone_lib="NCI CGAP_Brn67"

/lab_host="DH10B"

/note="Vector: PCMV-SPOrt6"

49..1398

/codon_start=1

/product="clusterin (complement lysis inhibitor, SP-40, 40,

sulfated glycoprotein 2, testosterone-repressed prostate

message 2, apolipoprotein J)"

/protein_id="AA019588.1"

/db_xref="GI:18043615"

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SLENDROQTHMDVMDHFSRASSIIIDELFODRFTREPQDTYHYLPFSLPHRPHF

FPKSRIVSRSLMPEFSEYELNFMHAFQPELEMIHBAQOAMDIHFSPAFQHPFEIR

EGDDRTVCREIRHNSTGCLRKMDCCDKREILSVDCSTNNPSQAKLRRELDSELOVA

RLTRKYNELKSYOKMKMLNTSLLLEOLNEOPNMYSRLANLTGEGDYLYLEVTYASH

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BASE COUNT

423 a 486 c 439 g 310 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 21; DB 9; Length 1658;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtctgagaccgtctgctc 21

|||||

Db 135 ATTGCTGAGACCGTCTGCTC 115

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RESULT 6

LOCUS HSCSP40 1676 bp mRNA linear PRI 22-MAR-1995

DEFINITION Human SP-40, 40 mRNA for complement-associated protein SP-40, 40

alpha-1 and beta-1 chain.

ACCESSION X14723

VERSION X14723.1 GI:30250

KEYWORDS complement-associated protein; serum protein; SP-40, 40 gene.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1676)

Kirsbaum, L.

Direct Submission

Submitted (17-MAR-1989) Kirsbaum L., The University of Melbourne,

The Preclinical Centre, School of Veterinary Science, Parkville

Victoria 3052, Australia

2 (bases 1 to 1676)

Kirsbaum, L., Sharpe, J.A., Murphy, B., d'Apice, A.J., Classon, B.,

Hudson, P. and Walker, I.D.

Molecular cloning and characterization of the novel, human

complement-associated protein, SP-40, 40: a link between the

complement and reproductive systems

EMBO J. 8 (3), 711-718 (1989)

89251601

Clin. Invest. 81:1858-1864(1988).

location/Qualifiers

1..1676

/organism="Homo sapiens"

/db_xref="taxon:9606"

FEATURES

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 48.1397
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 SLENDROOHTMLDVMODHFSRASSIIDELFQDFREPQDYYHYLPFLPRRHF
 FPKRSIRVSLMPSPYEPPLNFHAMQOPLEMIHEAOQANDIHFSAPARHPTEIR
 EGDDRTVCREIRHNSGICLRMKDQCKREITISVDCSTNNPQAKLRRLDLSLOVA
 ERLTRYNELKSTQMKMLNSSLLEQLNQFMVSKLANLTQGEDQYLRVTVASH
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 729..1394
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 1622..1627
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 436 a 488 c 437 g 315 t

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Oy 1 attgctgagaccgtctgctc 21
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 Db 134 ATTGCTGAGACCGTCTGCTC 114

RESULT 7
 AX202086/c
 LOCUS AX202086 1678 bp DNA linear PAT 30-AUG-2001
 DEFINITION Sequence 16 from Patent WO0153531.
 ACCESSION AX202086
 VERSION AX202086.1 GI:15391872
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1678)
 Philpard, D., Vasanthakumari, G., Dotson, S. and Ma, X.J.
 Osteoarthritis tissue derived nucleic acids, polypeptides, vectors,
 and cells
 JOURNAL Patent: WO 0153531-A 16 26-JUL-2001;
 Pharmacia Corporation (US)

FEATURES
 source
 1..1678
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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Query Match 100.0%; Score 21; DB 6; Length 1676;
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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 attgctgagaccgtctgctc 21
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 Db 156 ATTGCTGAGACCGTCTGCTC 136

RESULT 8
 BC010514/c
 LOCUS BC010514 1684 bp mRNA linear PRI 12-JUL-2001
 DEFINITION Homo sapiens, clusterin (complement lysis inhibitor, SP-40/40,
 sulfated glycoprotein 2, testosterone-repressed prostate message 2,
 apolipoprotein J), clone MGC:18080 IMAGE:4150452, mRNA, complete
 cds

ACCESSION BC010514
 VERSION BC010514.1 GI:14714740
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1684)
 Strausberg, R.
 Direct Submission
 Submitted (10-JUL-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: villalob@bcm.tmc.edu
 Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAC Plates: 19 Row: 0 Column: 12.
 Location/Qualifiers
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 /clone_id="NCI CGAP_Brn64"
 /lab_host="DH10B"
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 message 2, apolipoprotein J)"
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 /db_xref="GI:14714741"

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 FPKRSIRVSLMPSPYEPPLNFHAMQOPLEMIHEAOQANDIHFSAPARHPTEIR
 EGDDRTVCREIRHNSGICLRMKDQCKREITISVDCSTNNPQAKLRRLDLSLOVA
 ERLTRYNELKSTQMKMLNSSLLEQLNQFMVSKLANLTQGEDQYLRVTVASH
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BASE COUNT 433 a 493 c 448 g 310 t
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 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 attgctgagaccgtctgctc 21

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Db 155 ATTGCTGAGACCGCTGCTGTC 135

RESULT 9
LOCUS HUMTRPM2A1/c 7610 bp DNA linear PRI 23-AUG-1996
DEFINITION Human TRPM-2 protein gene, exons 1,2 and 3.
ACCESSION M63376
VERSION M63376.1 GI:292838
KEYWORDS TRPM-2 protein.
SEGMENT 1 of 4
SOURCE Human DNA.
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Wong,P., Pineault,J., Lakin,J., Taillefer,D., Leger,J., Wang,C.
and Tenniswood,M.
TITLE Genomic organization and expression of the rat TRPM-2 (clusterin)
JOURNAL J. Biol. Chem. 268 (7), 5021-5031 (1993)
MEDLINE 93168813
REFERENCE 2 (bases 1 to 7610)
AUTHORS Wong,P., Taillefer,D., Lakin,J., Pineault,J., Chader,G. and
Tenniswood,M.
TITLE Molecular characterization of human TRPM-2/clusterin, a gene
associated with sperm maturation, apoptosis and neurodegeneration
JOURNAL Eur. J. Biochem. 221 (3), 917-925 (1994)
MEDLINE 94237156
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/number=3
BASE COUNT 1660 a 1994 c 2055 g 1899 t 2 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtctgagaccgtctgctc 21
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Db 5624 ATTGCTGAGACCGCTGCTGTC 5604

RESULT 10
LOCUS AF235104/c 175382 bp DNA linear PRI 06-FEB-2002
DEFINITION Homo sapiens chromosome 8 clone GSI-251107 map 8p12, complete
sequence.
ACCESSION AF235104
VERSION AF235104.3 GI:18543385
KEYWORDS HTG: HTGS_FULFLOP; HTGS_ACTIVIFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 175382)
AUTHORS Men,G., Reichwald,K., Baumgart,C., Taudin,S., Baumgart,C. and
Platzer,M.
TITLE Chromosome 8 genomic sequence
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 175382)
AUTHORS Reichwald,K., Menzel,U., Dettle,M., Baumgart,C., Jahn,N., Men,G.,
Schillhabel,M. and Kosenthal,A.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE 3 (bases 1 to 175382)
AUTHORS Genome Sequencing Center Jena.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstr. 11, Jena 07745, Germany
REFERENCE 4 (bases 1 to 175382)
AUTHORS Men,G. and Platzer,M.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT On Feb 6, 2002 this sequence version replaced gi:1852056.

Genome Center
Center: Institute of Molecular Biotechnology
Center code: IMB
Web site: <http://genome.imb-jena.de/>
Contact: gscl-submit@genome.imb-jena.de

Project Information
Center project name: H342
Center clone name: GSI-251107

Summary Statistics
Sequencing vector: M13; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 172785 bases at least Q40
Consensus quality: 174289 bases at least Q30
Consensus quality: 174952 bases at least Q20
Quality coverage: 6.88 x in Q20 bases; sum-of-contigs

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality 10.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

Location/Qualifiers
source 1..175382
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8p12"
/clone="GSI-251107"
BASE COUNT 46563 a 38626 c 38604 g 51589 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 175382;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtctgagaccgtctgctc 21
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Db 173484 ATTGCTGAGACCGCTGCTGTC 173464

RESULT 11
LOCUS AC025192/c 187453 bp DNA linear HTG 13-MAY-2001
DEFINITION Homo sapiens chromosome 8 clone RP11-509E2 map 8, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
ACCESSION AC025192
VERSION AC025192.3 GI:12313839
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 187453)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 8, clone RP11-509E2
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 187453)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., DeRubeis, K., Dewar, K., Diaz, J., S.,
Dodge, S., Domino, M., Doyle, M., Ferrel, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., C., Iliev, I., Johnson, R., Jones, C., Kan, L., Karatas, A.,
Klein, J., Larocque, K., Lamazares, R., Landers, T., Lechoczy, J.,
Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R.,
Meidrum, J., Menus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, T., M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Teafaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (07-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center code: W1BR
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L5592
Center clone name: 509E2

Summary Statistics
Sequencing vector: M13; M77815; 48% of reads
Sequencing vector: Plasmid; n/a; 52% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 185120 bases at least Q40
Consensus quality: 185533 bases at least Q30
Insert size: 175000; agarose-IP
Insert size: 186853; sum-of-coverage
Quality coverage: 8.3 in Q20 bases; agarose-IP
Quality coverage: 8.3 in Q20 ba.

NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 17773: contig of 17773 bp in length
* 17774 17873: gap of 100 bp
* 17874 20278: contig of 2405 bp in length
* 20279 20378: gap of 100 bp
* 20379 35742: contig of 15364 bp in length
* 35743 35842: gap of 100 bp
* 35843 65413: contig of 29571 bp in length
* 65414 65513: gap of 100 bp
* 65514 112793: contig of 47280 bp in length

FEATURES
source
* 112794 112893: gap of 100 bp
* 112894 150031: contig of 37138 bp in length
* 150032 150131: gap of 100 bp
* 150132 187453: contig of 37322 bp in length.
Location/Qualifiers
1. 187453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8"
/clone="RP11-509E2"
/clone_lib="RP11-509E2 Human Male BAC"
1. 17773
/note="assembly_fragment"
clone_end:sp6
vector_side:left
1874. 20278
/note="assembly_fragment"
20379. 35742
/note="assembly_fragment"
35843. 65413
/note="assembly_fragment"
65514. 112793
/note="assembly_fragment"
112894. 150031
/note="assembly_fragment"
150132. 187453
/note="assembly_fragment"
clone_end:t7
vector_side:right

BASE COUNT 51878 a 43372 c 44058 g 47545 t 600 others
ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 187453;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgtctgagacgctgtgctc 21
|||||
Db 124941 ATGTCTGAGACCGTGTGCTC 124921

RESULT 12
AF311103/C 234431 bp DNA linear PRI 06-FEB-2002
LOCUS Homo sapiens chromosome 8 clone SCB-212e3 map 8p12, complete
DEFINITION
sequence.
ACCESSION AF311103
VERSION AF311103.3 GI:18542957
KEYWORDS HTG; HTGS_FUILLTOP; HTGS_ACTIVEFPT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 234431)
Wen, G., Bleischmidt, K., Baumgart, C., Taudin, S., Baumgart, C. and
Platzer, M.

REFERENCE 1
AUTHORS Chromosome 8 genomic sequence
JOURNAL Unpublished
TITLE 2 (bases 1 to 234431)
REFERENCE Bleischmidt, K., Jandrig, B., Baumgart, C., Detle, M., D., Jahn, N.,
Menzel, U., Schilhabel, M.B., Wen, G., Taudien, S. and Rosenthal, A.
JOURNAL Direct Submission
TITLE Submitted (04-OCT-2000) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
3 (bases 1 to 234431)
Wen, G. and Platzer, M.

REFERENCE 2
AUTHORS Submitted (06-FEB-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
JOURNAL On Feb 6, 2002 this sequence version replaced gi:14389409.
COMMENT ----- Genome Center

Center: Institute of Molecular Biotechnology
 Center code: IMB
 Web site: <http://genome.imb-jena.de/>
 Contact: gsci-submit@genome.imb-jena.de
 ----- Project Information -----
 Center project name: H319
 Center clone name: SCB-212e3
 ----- Summary Statistics -----
 Sequencing vector: M13: 100% of reads
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap: version 0.990329
 Consensus quality: 234404 bases at least Q40
 Consensus quality: 234413 bases at least Q30
 Consensus quality: 234428 bases at least Q20
 Quality coverage: 5.81 x in Q20 bases; sum-of-contrigs

 Sequence Quality Assessment:
 This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

 FEATURES
 Source Location/Qualifiers
 1. 234431
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8p12"
 /clone="SCB-212e3"
 BASE COUNT 62993 a 56257 c 55890 g 59291 t
 ORIGIN
 Query Match 100.0%; Score 21; DB 9; Length 234431;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 atgtctgagacgctctgctc 21
 ||||||||||||||||||||
 Db 14062 ATGTCTGAGACGCTCTGCTC 14042
 RESULT 13
 AC000360 136131 bp DNA linear PRI 03-JAN-2001
 LOCUS Homo sapiens Chromosome 2 BAC Clone 376a1, complete sequence.
 DEFINITION AC000360
 ACCESSION AC000360.35 GI:12018422
 VERSION
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 136131)
 Mcdermid,H.E.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 136131)
 Kim,U.-J. and Simon,M.I.
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 136131)
 Crabtree,J.S. and Roe,B.A.
 JOURNAL Homo sapiens Chromosome 2 BAC Clone 376a1
 TITLE Unpublished
 REFERENCE 4 (bases 1 to 136131)
 Lanttu,L. and Roe,B.A.
 JOURNAL Direct Submission
 TITLE Submitted (08-MAR-1997) Department of Chemistry And Biochemistry,
 JOURNAL The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA

REFERENCE 5 (bases 1 to 136131)
 Crabtree,J.S., Mcdermid,H.E., Kim,U.-J., Simon,M.I. and Roe,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (03-JAN-2001) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 On Jan 3, 2001 this sequence version replaced gi:12000483.
 COMMENT Location/Qualifiers
 source 1. 136131
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /clone="376a1"
 BASE COUNT 37449 a 29927 c 29780 g 38975 t
 ORIGIN
 Query Match 84.8%; Score 17.8; DB 9; Length 136131;
 Best Local Similarity 90.5%; Pred. No. 50;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 atgtctgagacgctctgctc 21
 ||||||||||||||||||||
 Db 62757 ATGTCTGAGACGCTCTGCTC 62777
 RESULT 14
 AC092103 171830 bp DNA linear HTG 24-JAN-2002
 LOCUS Homo sapiens chromosome 2 clone RP11-143D11, WORKING DRAFT
 DEFINITION AC092103
 ACCESSION AC092103
 VERSION AC092103.4 GI:18308811
 KEYWORDS HTGS; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 171830)
 Waterston,R.H.
 JOURNAL The sequence of Homo sapiens clone
 REFERENCE 2 (bases 1 to 171830)
 Waterston,R.H.
 JOURNAL Direct Submission
 TITLE Submitted (21-JUN-2001) Genome Sequencing Center, Washington
 JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Jan 24, 2002 this sequence version replaced gi:16799048.
 COMMENT ----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 Contact: submissions@wustl.wustl.edu
 ----- Project Information -----
 Center project name: H_NH0143D11
 ----- Summary Statistics -----
 Sequencing vector: M13: 0%
 Sequencing vector: plasmid: 100%
 Chemistry: Dye-Primer ET: 0% of reads
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap: version 0.990319
 Consensus quality: 168467 bases at least Q40
 Consensus quality: 168467 bases at least Q30
 Consensus quality: 168732 bases at least Q20
 Insert size: 176000; agarose-fp
 Insert size: 170339; sum-of-contrigs
 Quality coverage: 8.19 in Q20 bases; agarose-fp
 Quality coverage: 7.96 in Q20 bases; sum-of-contrigs

 * NOTE: This is a 'working draft' sequence. It currently

* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1149: contig of 1149 bp in length
* 1150 1249: gap of unknown length
* 1250 2446: contig of 1197 bp in length
* 2447 2546: gap of unknown length
* 2547 2937: contig of 391 bp in length
* 2938 3037: gap of unknown length
* 3038 23810: contig of 20773 bp in length
* 23811 23910: gap of unknown length
* 23911 27801: contig of 3891 bp in length
* 27802 32273: gap of unknown length
* 32274 32373: gap of unknown length
* 32374 37772: contig of 5399 bp in length
* 37773 37872: gap of unknown length
* 37873 51582: contig of 13710 bp in length
* 51583 51682: gap of unknown length
* 51683 67875: contig of 16193 bp in length
* 67876 67975: gap of unknown length
* 67976 86365: contig of 18389 bp in length
* 86365 86464: gap of unknown length
* 86465 104764: contig of 18200 bp in length
* 104765 171830: contig of 67066 bp in length.
* Location/Qualifiers
1. 171830

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-143D11"
1. 1149
misc_feature
/note="assembly_name:Contig15"
1250. 2446
misc_feature
/note="assembly_name:Contig28"
2547. 2937
misc_feature
/note="assembly_name:Contig41"
3038. 23810
misc_feature
/note="assembly_name:Contig62"
vector_end:17
23911. 27801
misc_feature
/note="assembly_name:Contig55"
27902. 32273
misc_feature
/note="assembly_name:Contig56"
32374. 37772
misc_feature
/note="assembly_name:Contig57"
37873. 51582
misc_feature
/note="assembly_name:Contig58"
51683. 67875
misc_feature
/note="assembly_name:Contig59"
67976. 86364
misc_feature
/note="assembly_name:Contig60"
86465. 104664
misc_feature
/note="assembly_name:Contig61"
104765. 171830
misc_feature
/note="assembly_name:Contig63"
BASE COUNT 47788 a 37462 c 36363 g 49114 t 1103 others
ORIGIN

Query Match 84.88: Score 17.8; DB 2: Length 171830;
Best Local Similarity 90.5%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 attgtcagagcgtctgtc 21
|||||
Db 122060 ATTGTGAGACATTTGTC 122080

RESULT 15

HS125H2
LOCUS

HS125H2 173513 bp DNA linear PRI 12-DEC-1999

DEFINITION

Human DNA sequence from clone CTA-125H2 on chromosome 22q11.12
Contains part of the gene for a novel protein similar to KIAA0216
and myosin heavy chain, ESTs, GSSs and a Cpg Island, complete
sequence.

ACCESSION

Z98949.1 GI:3168990

VERSION

HTG: Cpg Island; KIAA0216; myosin.
human.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 173513)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Lloyd, P.

TITLE

Direct Submission

JOURNAL

Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonequests@sanger.ac.uk

COMMENT

On May 30, 1998 this sequence version replaced gi:2558540.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.

This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr22>
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
from the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
from the human BAC library described in U-J. Kim et al. (1996)
Genomics 34, 213-218.
VECTOR: pBAC108L

This sequence is the entire insert of clone CTA-125H2 The start of
this sequence overlaps with sequence AL000000. The end of this
sequence overlaps with sequence AL000000.

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
/map="q11.12"
/clone="CTA-125H2"
/clone_id="CT978SK-A1"
231. 371
repeat_region
/note="Mir repeat: matches 40. 192 of consensus"
gene
/gene="DK125H2.1"
/gene<563. 710. 9002. 9161.11367. 11550.12697. 12919.
16737. 16846.33587. 33652.39553. 39681.41456. 41599.
43226. 43315.56023. 56142.56571. 56679.60423. 60547.
63574. 63728.67880. 68003.68898. 69098.73589. 73699.
76213. 76317.86524. 86676.111403. 111516.112978. 113094.
115633. 115716.117513. 117689.120445. 120630.
157629. 157759)
/gene="DK125H2.1"
16737. 16846.33587. 33652.39553. 39681.41456. 41599.
43226. 43315.56023. 56142.56571. 56679.60423. 60547.
63574. 63728.67880. 68003.68898. 69098.73589. 73699.
76213. 76317.86524. 86676.111403. 111516.112978. 113094.

115633. .115716,117513. .117669,120445. .120630,
157629. .>157759)
/gene="bk125H2.1"
/note="match: CDNAS: Em:D86970
match: ESTs: Em:A18346 Em:AA504934 Em:R41006
match: proteins: Tr:060772 Tr:092614
match: genomic DNA: Em:H55072 Em:H55541 Em:H55303"
/codon_start=1
/evidence=not experimental
/product="bk125H2.1 (novel protein similar to KIA0216 and
myosin heavy chain)"
/protein_id="CAB11606.2"
/db_xref="SPTREMBL:060772"
/db_xref="GI:6572182"
/translation="VRLPAGGAGDARGLFWLDEEVHVGSSDVLRLCAAEFK
GATGSSSALRTCEPLGCEHOLGMDPVAYDTGLHFAKNLSALAPOLHOSK
RRELRLFOARAKLPPVCAVAGLEAGTSOALORSRVRRTPSAARRAPGSOI
KIOMALTSMIKRSRLHITICTYPNPVYESGSGESPPOPRDRPGAGPLADIP
ALVOLAGHILRLRITGADHMGILFRROQVLDAPLRLKLSIBGLDERKA
VEELLETDLEKKAAGVAGSOFKAGVISLKEQREKLSQSIVLQAACKGSLRSQ
EERKLRIRLAOCIOKNVAVFLAKDMPWQLGSLQPLSATIGTEOLRAKEELT
TLRRLEKSEKLRNELRONTDLSEKIADLDERFEGDVAQVLSERAEKLA
PREVOELKSEHOYKRLGDYVKOLEPAQKIQLNDELRRTGADWOMRFECAOM
NEFLRRLOQCEERLSELTARKELEOKIGLGSAYGAKMAHOLKRCNHLTOL
DPCVLLENOSRHELEKOKKRPDLOALAGSEVPFEGKLRKRVQENSVRMEISOL
OOOLKOKREBASQLQOYEMIDHKRELSPSGENGVAGLERKLEKSSALEOK
IOSQDENTIKOLBQLEKRFLEIEKMKOMKDEDEEBLEVRROSCORHLQLEMO
LSEYEEKOMLHEKODLEGILGICDQIGRIDVERKRLRLRTHALISVOLL
GTMEDEKTSVSEKLELVHQSODESEAKCEALTKOVLNADLESMSHEENATKRS
LVDEOLYRLFQEKADLKRIDEDDLNEMOKHDKDIASADIGIOLELODEKA
KKEKHRLKOGGOSNRSLSTYLOLVAKOMREYLEOSTVRAIYSROEAVICLEKRT
EPOKVOIKRFEVLVIRLSDSLKMGSELSOATSEOSTRESSQYTORLEEKLEK
LVQREASRRCKMEKYEVEELAVRQTLQTDLETSTRADLQALAEVASSDSOTE
"
855. .924
/note="L2 repeat: matches 2686. .2749 of consensus"
1660. .1713
/note="18 copies 3 mer tga 72 conserved"
1946. .2233
/note="AluSq repeat: matches 1. .287 of consensus"
2234. .2278
/note="15 copies 3 mer taa 100 conserved"
2362. .2423
/note="L2 repeat: matches 2679. .2741 of consensus"
2489. .2836
/note="L2 repeat: matches 1257. .1637 of consensus"
3136. .3334
/note="L1PA11 repeat: matches 5960. .6165 of consensus"
3384. .3475
/note="23 copies 4 mer atat 72 conserved"
3392. .3473
/note="41 copies 2 mer at 76 conserved"
3483. .3743
/note="AluSq repeat: matches 24. .283 of consensus"
3750. .4067
/note="MER7A repeat: matches 1. .329 of consensus"
4073. .4252
/note="45 copies 4 mer tgtg 73 conserved"
4077. .4250
/note="87 copies 2 mer tg 73 conserved"
4253. .4552
/note="75 copies 4 mer gtgt 75 conserved"
4555. .4640
/note="ORSL repeat: matches 189. .274 of consensus"
5228. .5472
/note="L2 repeat: matches 2434. .2693 of consensus"
5497. .5647
/note="L2 repeat: matches 2286. .2442 of consensus"
7015. .7116
/note="L2 repeat: matches 2561. .2669 of consensus"
7200. .7239
/note="L2 repeat: matches 2580. .2619 of consensus"
7658. .7961

/note="AluSq repeat: matches 1. .305 of consensus"
8081. .8163
/note="L2 repeat: matches 2619. .2710 of consensus"
8230. .8419
/note="MIR repeat: matches 57. .245 of consensus"
complement(9497. .9973)
/note="match: GSS: Em:AQ00189"
9769. .9950
/note="MIR repeat: matches 54. .250 of consensus"
10305. .10353
/note="MIR repeat: matches 97. .149 of consensus"
10504. .10811
/note="AluSc repeat: matches 1. .308 of consensus"
11638. .11776
/note="MIR repeat: matches 46. .188 of consensus"
12067. .12375
/note="AluSc repeat: matches 1. .309 of consensus"
12426. .12515
/note="MIR repeat: matches 47. .136 of consensus"
13064. .13180
/note="MIR repeat: matches 20. .134 of consensus"
complement(13160. .13420)
/note="match: GSS: Em:AQ00982"
13204. .13243
/note="10 copies 4 mer acac 95 conserved"
13246. .13314
/note="L1PA7 repeat: matches 6057. .6125 of consensus"
13444. .13868
/note="bk125H2.1"
/note="match: GSS: Em:AQ00882"
13447. .13881
/gene="bk125H2.1"
/note="match: GSS: Em:AQ409072"
13449. .13908
/gene="bk125H2.1"
/note="match: GSS: Em:AQ819687"
13535. .13778
/note="L2 repeat: matches 2273. .2554 of consensus"
14793. .14826
/note="L2 repeat: matches 2695. .2728 of consensus"
14901. .15097
/note="MIR repeat: matches 4. .221 of consensus"
15155. .15308
/note="MIR repeat: matches 31. .190 of consensus"
15636. .15831
/note="MIR repeat: matches 44. .262 of consensus"
15848. .16027
/note="AluB repeat: matches 112. .297 of consensus"
16056. .16185
/note="L2 repeat: matches 2355. .2487 of consensus"
16918. .17021
/note="AluJ/FLAM repeat: matches 2. .101 of consensus"
17444. .17555
/note="L2 repeat: matches 2363. .2475 of consensus"
17623. .17669
/note="L2 repeat: matches 2665. .2710 of consensus"
17860. .17971
/note="MIR repeat: matches 77. .192 of consensus"
Query Match 84.8%; Score 17.8; DB 9; Length 173513;
Best Local Similarity 90.5%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 attgtctagacgctgctgc 21
Db 167590 ATTGCTGAGACTTCTGCTG 167610
Search completed: May 17, 2002, 16:04:32
Job time: 16132 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 15:25:38 ; Search time 3628.41 Seconds
(without alignments)
78.116 Million cell updates/sec

Title: US-09-913-325-12

Perfect score: 21

Sequence: 1 gctggcgaggttgaggagcct 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	121	10	H84500 yv02d12.s1
2	21	100.0	121	10	R93611 yq38d11.s1
3	21	100.0	135	10	T53781 yb3e02.s1
4	21	100.0	143	10	BE765434 IL3-NT010
5	21	100.0	145	9	AM904670 RC1-NN106
6	21	100.0	146	9	AA738045 nx15f08.s
7	21	100.0	151	9	AA434384 zw31h11.s
8	21	100.0	151	10	B1055204 PM2-GN049
9	21	100.0	153	10	B1040715 PM2-NT023
10	21	100.0	157	10	B1040715 PM2-NT023
11	21	100.0	159	10	B1467181 IC19a12.x
12	21	100.0	169	9	A1523434 PM2-NT023
13	21	100.0	169	9	A1691105 tx90g01.x
14	21	100.0	171	10	BF897129 IL0-NT021
15	21	100.0	171	10	BF919288 IL0-NT017
16	21	100.0	172	9	AA235650 z536f04.s
17	21	100.0	172	10	BF932077 PM2-NT023

18	21	100.0	174	9	AA635704 nt33e02.s
19	21	100.0	174	10	BE702836
20	21	100.0	174	10	BF374244 MRL-SN006
21	21	100.0	176	10	B1040542 PM2-NT023
22	21	100.0	176	10	BF364496 QV2-NN107
23	21	100.0	177	10	B1040538 PM2-NT023
24	21	100.0	179	9	AM868593 MRL-SN006
25	21	100.0	179	10	B1040710 PM2-NT023
26	21	100.0	181	10	B1040535 PM2-NT023
27	21	100.0	182	9	AM868587 MRL-SN006
28	21	100.0	184	9	AA433884 zw31h11.r
29	21	100.0	185	10	R83374 yp05f05.s1
30	21	100.0	187	9	AM897945 RC3-NN006
31	21	100.0	187	10	BE765800 IL3-NT010
32	21	100.0	187	10	BE766185 IL3-NT010
33	21	100.0	190	10	BF749857 CM3-BN038
34	21	100.0	193	10	B1040729 PM2-NT023
35	21	100.0	195	9	AM904698 RC1-NN106
36	21	100.0	196	10	BF749861 PM2-NT023
37	21	100.0	196	10	B1040731 PM2-NT023
38	21	100.0	196	10	B1055202 PM2-NT049
39	21	100.0	198	9	AM243998 x448e10.x
40	21	100.0	198	9	AM868592 MRL-SN006
41	21	100.0	199	9	AM904691 RC1-NN106
42	21	100.0	199	10	BF823349 PM2-NT005
43	21	100.0	200	10	B1055200 PM2-GN049
44	21	100.0	201	9	AM897949 RC3-NN006
45	21	100.0	201	10	B1040531 PM2-NT023

ALIGNMENTS

RESULT 1
H84500 121 bp mRNA linear EST 13-NOV-1995
LOCUS yv02d12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
DEFINITION IMAGE:241559 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);,
mRNA sequence.
H84500
H84500.1 GI:1063171
EST.

KEYWORDS

ORGANISM

REFERENCE

1 (bases 1 to 121)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Ten, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

TITLE

JOURNAL

COMMENT

FEATURES

source
High quality sequence starts: 1
Source: IMAGE Consortium, LBL
This clone is available royalty-free through LBL; contact the
IMAGE Consortium (info@image.lbl.gov) for further information.
Trace considered overall poor quality
Seq primer: Promega-21m13
High quality sequence stop: 1.
location/Qualifiers
1..121
/organism="Homo sapiens"
/db_xref="GDB:3790692"
/db_xref="taxon:9606"
/clone="IMAGE:241559"

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/clone_lib="Soares fetal liver spleen INFUS"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pRT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I oligo(dT) primer
(5' AACTGAGAGATTAAATTAAGATCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pRT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      27 a      20 c      45 g      20 t      9 others
ORIGIN

Query Match      100.0%; Score 21; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 2, 1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 gctggcgaggttggtggcct 21
        |||
Db      95 GCTGGCGGAGTGTGGGCGCT 115

RESULT 2
R93611      121 bp      mRNA      linear      EST 29-ANG-1995
LOCUS      y936d11.s1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone
DEFINITION IMAGE:198069 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);,
          mRNA sequence.
ACCESSION      R93611
VERSION      R93611.1
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 121)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Merritt,M., Parsons,J.,
Ritkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1368
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL.
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1368 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
1. 121
/organism="Homo sapiens"
/db_xref="GDB:3767119"
/db_xref="taxon:9606"
/clone="IMAGE:198069"
/clone_lib="Soares fetal liver spleen INFUS"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pRT73D (Pharmacia)

```

```

with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
(5' AACTGAGAGATTAAATTAAGATCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pRT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      23 a      22 c      50 g      23 t      3 others
ORIGIN

Query Match      100.0%; Score 21; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 2, 1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 gctggcgaggttggtggcct 21
        |||
Db      85 GCTGGCGGAGTGTGGGCGCT 105

RESULT 3
T53781      135 bp      mRNA      linear      EST 06-FEB-1995
LOCUS      yb83e02.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
DEFINITION IMAGE:77786 3' similar to gb:X14723 CLUSTERIN PRECURSOR
          (HUMAN), mRNA sequence.
ACCESSION      T53781
VERSION      T53781.1
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 135)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chappelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,M., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Ritkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierly-Meg,J., Trevasakis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Merritt,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1905
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL. This clone is available royalty-free
through LNL; contact the IMAGE Consortium (info@image.lnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 1905 Std Error: 0.00
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
1. 135
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/db_xref="GDB:497531"
/db_xref="taxon:9606"
/clone="IMAGE:77786"
/clone_lib="Stratagene liver (#937224)"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/notes="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGACGAG 3' -3' adaptor sequence: 5'

```

BASE COUNT	30 a	23 c	48 g	32 t	2 others
ORIGIN	CTCGAGTGTGTTTTTTTTTTTTTTT 3'				
Query Match	100.0%; Score 21; DB 10; Length 135;				
Best Local Similarity	100.0%; Pred. No. 2.2e+02;				
Matches	21: Conservative	0: Mismatches	0: Indels	0: Gaps	0:
QY	1 gctggcgagagtggtgggacct 21				
Db	110	GCTGGCGAGAGTGGGGGCGCT 130			
RESULT	4				
LOCUS	BE765434/c	143 bp	mRNA	linear	EST 19-SEP-2000
DEFINITION	IL3-NT0104-200500-144-G04 NT0104 Homo sapiens cDNA, mRNA sequence.				
ACCESSION	BE765434				
VERSION	BE765434.1 GI:10195358				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 143)				
AUTHORS	Nagai, M., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Dias Neto, E., Garcia Correia, R., Zago, M. A., Bordin, S., Costa, F. F., Goldmann, G. H., Carvalho, A. F., Matsukuma, A., Bata, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
MEDLINE	20020663				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/ICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-IL3-NT0104-200500-144-G04&t3=2000-05-20&t4=1) Seq primer: puc 18 forward Seg primer: puc 18 forward High quality sequence start: 8 High quality sequence stop: 143. Location/Qualifiers 1. 143 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lid="NT0104" /dev_strage="Adult" /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
BASE COUNT	27 a	65 c	28 g	23 t	
ORIGIN					
Query Match	100.0%; Score 21; DB 10; Length 143;				
Best Local Similarity	100.0%; Pred. No. 2.2e+02;				
Matches	21: Conservative	0: Mismatches	0: Indels	0: Gaps	0:
QY	1 gctggcgagagtggtgggacct 21				

Db	102	GCTGGCGGAGTTGGGGGCTT	92	
RESULT	5			
LOCUS	AW904670		145 bp	mRNA
DEFINITION	RC1-NN1062-260400-011-a09 NN1062 Homo sapiens cDNA, mRNA sequence.			
ACCESSION	AW904670			
VERSION	AW904670.1	GI:8068784		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. J., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matukuma, A., Bata, G. S., Simpson, D. H., Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J. J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20202663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=6t2-RC1-NN1062-260400-011-a09&f3=2000-04-26&f4=1) Seq primer: puc 18 forward High quality sequence start: 34 High quality sequence stop: 145.			
FEATURES	Location/Qualifiers			
Source	1..145 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="NN1062" /dev_stage="Adult" /note="Organ: nervous normal; Vector: puc18; Site:1; Smal: Site:2; Smal: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
BASE COUNT	20 a 31 c 61 g 33 t			
ORIGIN				
Query Match	100.0%;	Score 21;	DB 9;	Length 145;
Best Local Similarity	100.0%;	Pred. No. 2.2e+02;		
Matches	21; Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
Qy	1 gctggcgagcttgaggcct 21			
Db	50 GCTGGCGGAGTTGGGGGCTT 70			
RESULT	6			
LOCUS	AA738045		146 bp	mRNA
DEFINITION	nx15f08.s1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1256199 3' similar to gp:xl4723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.			
ACCESSION	AA738045			

VERSION AA738045.1 GI:2768802
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 146)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rt@mail.nih.gov
 Tissue procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbp/image/image.html

FEATURES
 source
 1..146
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1256199"
 /clone_lib="NCI-CGAP-GC3"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="vector: pT73D-Pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 32 a 26 c 54 g 34 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgaggttggggcct 21
 ||||||||||||||||
 Db 106 gctggcgaggttggggcct 126

RESULT 7
 LOCUS AA434384 151 bp mRNA linear EST 29-MAY-1997
 DEFINITION zw1h11.s1 Soares ovary tumor NbHOT Homo sapiens CDNA clone
 IMAGE:770949.3' similar to gb:U4723 CLUSTERIN PRECURSOR (HUMAN);
 mRNA sequence.
 AA434384
 AA434384.1 GI:2139298
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 151)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.

TITLE Washu-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilison RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40m3 fwd. Et from Amersham.
 Location/Qualifiers
 1..151
 /organism="Homo sapiens"
 /db_xref="GDB:5980822"
 /db_xref="taxon:9606"
 /clone_image="770949"
 /clone_lib="Soares ovary tumor NbHOT"
 /sex="female"
 /tissue_type="ovarian tumor"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site: 1; Not I; Site: 2; Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 32 a 27 c 56 g 36 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 151;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgaggttggggcct 21
 ||||||||||||||||
 Db 107 gctggcgaggttggggcct 127

RESULT 8
 LOCUS BI055204 151 bp mRNA linear EST 15-JUN-2001
 DEFINITION PM2-GN0495-050201-001-g05 GN0495 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BI055204
 VERSION BI055204.1 GI:14462734
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 151)
 AUTHORS Dias, Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-27070422
 Fax: +55-11-27070001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-GN0495-050201-001-g05&t3=2001-02-05&t4=1>)

Seq primer: puc 18 forward
 High quality sequence start: 7
 High quality sequence stop: 148.

FEATURES

SOURCE

1. 151

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="GN0495"

/dev_stage="Adult"

/note="Organ: Placenta,normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

24 a 32 c 61 g 34 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 151;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggggggagttggggcct 21
 |||
 61 GCTGGGGGAGTTGGGGCCT 81

Db 61 GCTGGGGGAGTTGGGGCCT 81

RESULT 9

BI040715

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

COMMENT

TITLE

JOURNAL

MEDLINE

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

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BASE COUNT 17 a 36 c 67 g 33 t

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RESULT 10

BI467181

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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BASE COUNT 17 a 36 c 67 g 33 t

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 |||
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Db 35 GCTGGGGGAGTTGGGGCCT 55

RESULT 10

BI467181

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

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MEDLINE

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BASE COUNT 17 a 36 c 67 g 33 t

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 35 GCTGGGGGAGTTGGGGCCT 55

Db 35 GCTGGGGGAGTTGGGGCCT 55

RESULT 10

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LOCUS

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BASE COUNT 17 a 36 c 67 g 33 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
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Db 35 GCTGGGGGAGTTGGGGCCT 55

RESULT 10

BI467181

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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BASE COUNT

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FEATURES

SOURCE

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 169)
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaaps-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmett-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.lnl.gov/dbip/image/image.html Insert Length: 869 Std Error: 0.00 Seq primer: -40up from Gibco.
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LOCUS	BF897129
DEFINITION	IL0-MT0215-281100-501-a11 MT0215 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BF897129
VERSION	BF897129.1 GI:12286588
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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1 (bases 1 to 171)	
Dias Neto,E.; Garcia Correa,R.; Verjowski-Almeida,S.; Briones,M.R.;	
Nagai,M.A.; da Silva,W.Jr.; Zago,M.A.; Bordin,S.; Costa,F.F.;	
Goldman,G.H.; Carvalho,A.F.; Matsumura,A.; Bala,G.S.; Simpson,D.H.;	
Brunstein,A.; deoliveira,P.S.; Bucher,P.; Jongeneel,C.V.; O'Hare	
M.J.; Soares,F.; Brentani,R.R.; Reis,L.F.; de Souza,S.J. and	
Simpson,A.J.	
Shoyun sequencing of the human transcriptome with ORF expressed	
sequence tags	
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
20202663	
Contact: Simpson A.J.G.	
Laboratory of Cancer Genetics	
Ludwig Institute for Cancer Research	
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,	
Brazil	
Tel.: +55-11-2704922	

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FEATURES
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            716 - Ludwig Institute for Cancer Research) profiles
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            34 t
BASE COUNT
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VERSION BP919288.1 GI:12315176
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 171)
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Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare
M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil)
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL06C2-IL0-MT0171
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Search completed: May 17, 2002, 15:25:40
 Job time: 14517 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 17:58:45 ; Search time 147.64 Seconds
(without alignments)
66.583 Million cell updates/sec

Title: US-09-913-325-12

Perfect score: 21

Sequence: 1 gctggcgagtggtgggacct 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 424068 segs, 234053524 residues

Total number of hits satisfying chosen parameters: 848136

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	US-60-365-384-115	Sequence 115, App
3	21	100.0	US-10-116-255-17	Sequence 17, Appl
4	16.4	78.1	US-10-125-086-9	Sequence 9, Appl
5	16.4	78.1	PCT-US02-01109-10	Sequence 10, Appl
6	16.4	78.1	PCT-US02-06990-10	Sequence 10, Appl
7	16.4	78.1	PCT-US02-08239-10	Sequence 10, Appl
8	16.4	78.1	PCT-US02-09135-10	Sequence 10, Appl
9	16.4	78.1	PCT-US02-09105-10	Sequence 10, Appl
10	16.4	78.1	PCT-US02-09188-10	Sequence 10, Appl
11	16.4	78.1	PCT-US02-09257-10	Sequence 10, Appl
12	16.4	78.1	PCT-US02-09370-10	Sequence 10, Appl
13	16.4	78.1	PCT-US02-09785-10	Sequence 10, Appl
14	16.4	78.1	PCT-US02-09922-10	Sequence 10, Appl
15	16.4	78.1	US-10-103-313-10	Sequence 10, Appl
16	16.4	78.1	US-10-102-627-10	Sequence 10, Appl
17	16.4	78.1	US-10-103-295-10	Sequence 10, Appl
18	16.4	78.1	US-10-105-299-10	Sequence 10, Appl
19	16.4	78.1	US-10-106-698-10	Sequence 10, Appl
20	16.4	78.1	US-10-102-806-846	Sequence 846, App
21	16.4	78.1	US-10-112-857-10	Sequence 10, Appl
22	16.4	78.1	US-10-115-123-10	Sequence 10, Appl
23	16.4	78.1	US-10-115-928-10	Sequence 10, Appl
24	16.4	78.1	US-10-116-016-10	Sequence 10, Appl
25	16.4	78.1	US-10-116-355-10	Sequence 10, Appl
26	16.4	78.1	US-10-004-860-10	Sequence 10, Appl

27	16.4	78.1	US-10-125-451-30	Sequence 30, Appl
28	16.4	78.1	US-10-125-540-10	Sequence 10, Appl
29	16.4	78.1	US-10-074-045-10	Sequence 10, Appl
30	16.4	78.1	PCT-US02-01109-5	Sequence 5, Appl
31	16.4	78.1	PCT-US02-06990-5	Sequence 5, Appl
32	16.4	78.1	PCT-US02-09239-5	Sequence 5, Appl
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36	16.4	78.1	PCT-US02-09257-5	Sequence 5, Appl
37	16.4	78.1	PCT-US02-09370-5	Sequence 5, Appl
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43	16.4	78.1	US-10-105-299-5	Sequence 5, Appl
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ALIGNMENTS

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; Sequence 227, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053, 375B
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 227
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-227

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; Sequence 115, Application US/60365384
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Zhao, Qing A.
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Meng, Gezhi
; TITLE OF INVENTION: Novel Nucleic Acids and
; Polypeptides

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; FILE REFERENCE: 814
; CURRENT APPLICATION NUMBER: US/60/365.384
; CURRENT FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: pf_FL-genes Version 6.0
; SEQ ID NO 115
; LENGTH: 1839
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (132)..(1316)
US-60-365-384-115
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; Sequence 17, Application US/10116255
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: Uncoupling Protein Polynucleotides, Polypeptides, and
; FILE REFERENCE: PTO09P1
; CURRENT APPLICATION NUMBER: US/10/116.255
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/685,897
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09534
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,701
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/142,821
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/149,448
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/164,751
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
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; TYPE: DNA
; ORGANISM: Homo sapiens
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; Sequence 9, Application US/10125086
; GENERAL INFORMATION:
; APPLICANT: MONTELABRO, Ronald
; APPLICANT: CRAIGO, Jodi K.
; APPLICANT: ISSEL, Charles
; APPLICANT: PUFFER, Bridget
; APPLICANT: HENNESSY, Kristina J.
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; APPLICANT: BROWN, Karen K.
; TITLE OF INVENTION: E1AV P26 DELETION VACCINE AND DIAGNOSTIC
; FILE REFERENCE: MONTELABRO ET AL.
; CURRENT APPLICATION NUMBER: US/10/125,086
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US/09/659,026A
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
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; LENGTH: 226
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; ORGANISM: IN VITROGEN
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; Sequence 10, Application PC/TUS0201109
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/01109
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/262,066
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-K
PCT-US02-01109-10
```

```
Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 2 ctggcgagagttgggggc 19
    ||||||||||||
Db 123 CTGGCGGAGTTAGGGGC 106
```

```
RESULT 6
PCT-US02-06990-10/c
; Sequence 10, Application PC/TUS0206990
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PF534PCT
; CURRENT APPLICATION NUMBER: PCT/US02/06990
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,214
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 256
```

```
;
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-KB
PCT-US02-06990-10
```

```
Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 ctgggcgaggttg9gggc 19
        |||1111111111111111
DB      123 CTGGCGCGAGTTAGGGGC 106
```

RESULT 7

```
PCT-US02-09239-10/c
; Sequence 10, Application PC/TUS0209239
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS953PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09239
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-KB
PCT-US02-09239-10
```

```
Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 ctgggcgaggttg9gggc 19
        |||1111111111111111
DB      123 CTGGCGCGAGTTAGGGGC 106
```

RESULT 8

```
PCT-US02-09135-10/c
; Sequence 10, Application PC/TUS0209135
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS956PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09135
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
```

```
;
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-K
PCT-US02-09135-10
```

```
Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 ctgggcgaggttg9gggc 19
        |||1111111111111111
DB      123 CTGGCGCGAGTTAGGGGC 106
```

RESULT 9

```
PCT-US02-09105-10/c
; Sequence 10, Application PC/TUS0209105
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS951PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09105
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 779
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-K
PCT-US02-09105-10
```

```
Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 ctgggcgaggttg9gggc 19
        |||1111111111111111
DB      123 CTGGCGCGAGTTAGGGGC 106
```

RESULT 10

```
PCT-US02-09188-10/c
; Sequence 10, Application PC/TUS0209188
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS952PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09188
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1732
; SOFTWARE: Patentln Ver. 2.0
```

```
; SEQ ID NO 10
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-KB
; OTHER INFORMATION: binding sites.
PCT-US02-09188-10
```

```
Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 ctgggcgaggttggggc 19
        |||
Db      123 CTGGCGGAGTTAGGGGC 106
```

```
RESULT 11
PCT-US02-09257-10/c
; Sequence 10, Application PC/TUS0209257
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS957PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09257
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 994
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-KB
; OTHER INFORMATION: binding sites.
PCT-US02-09257-10
```

```
*Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 ctgggcgaggttggggc 19
        |||
Db      123 CTGGCGGAGTTAGGGGC 106
```

```
RESULT 12
PCT-US02-09370-10/c
; Sequence 10, Application PC/TUS0209370
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS954PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09370
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1834
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-K
; OTHER INFORMATION: binding sites.
PCT-US02-09370-10
```

```
Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 ctgggcgaggttggggc 19
        |||
Db      123 CTGGCGGAGTTAGGGGC 106
```

```
RESULT 13
PCT-US02-09785-10/c
; Sequence 10, Application PC/TUS0209785
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS905PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09785
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Protein_Bind
; OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-K
; OTHER INFORMATION: binding sites.
PCT-US02-09785-10
```

```
*Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 ctgggcgaggttggggc 19
        |||
Db      123 CTGGCGGAGTTAGGGGC 106
```

```
RESULT 14
PCT-US02-09922-10/c
; Sequence 10, Application PC/TUS0209922
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS955PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09922
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
```

```

: NUMBER OF SEQ ID NOS: 1117
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10
: LENGTH: 256
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Protein_Bind
: OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-KB
: OTHER INFORMATION: binding sites.
PCT-US02-09922-10

```

```

Query Match          78.1%; Score 16.4; DB 1; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 2 ctggcgagagttgggac 19
    |||||
Db 123 CTGGCGGAGTTAGGGCC 106

```

```

RESULT 15
US-10-103-313-10/C
: Sequence 10, Application US/10103313
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P0207C1
: CURRENT APPLICATION NUMBER: US/10/103,313
: CURRENT FILING DATE: 2002-03-12
: NUMBER OF SEQ ID NOS: 653
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10
: LENGTH: 256
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic promoter for use in biological assays; includes NF-KB
: OTHER INFORMATION: binding sites.
US-10-103-313-10

```

```

Query Match          78.1%; Score 16.4; DB 6; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 2 ctggcgagagttgggac 19
    |||||
Db 123 CTGGCGGAGTTAGGGCC 106

```

Search completed: May 17, 2002, 17:58:46
Job time: 9180 sec

LENGTH: 21
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-12

Query Match 100.0%; Score 21; DB 37; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgaggttggggcct 21
|||||
DB 1 gctggcgaggttggggcct 21

RESULT 5
US-09-534-840-9475/C
Sequence 9475, Application US/09534840
GENERAL INFORMATION:
APPLICANT: Sellhame, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLEC
FILE REFERENCE: PD-1010 CIP
CURRENT APPLICATION NUMBER: US/09/534,840
CURRENT FILING DATE: 1992-07-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 13675
SOFTWARE: PERL Program
SEQ ID NO 9475
LENGTH: 166
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00589179
NAME/KEY: unsure
LOCATION: 64, 73, 121, 140, 152, 160, 163
OTHER INFORMATION: a, t, c, g, or other
US-09-534-840-9475

Query Match 100.0%; Score 21; DB 20; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgaggttggggcct 21
|||||
DB 27 gctggcgaggttggggcct 7

RESULT 6
US-60-033-401-581/C
Sequence 581, Application US/60033401
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
NUMBER OF SEQUENCES: 3552
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/033,401
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0297P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 581:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 2306438H1
US-60-033-401-581

Query Match 100.0%; Score 21; DB 42; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgaggttggggcct 21
|||||
DB 27 gctggcgaggttggggcct 7

RESULT 7
US-09-534-840-10418/C
Sequence 10418, Application US/09534840
GENERAL INFORMATION:
APPLICANT: Sellhame, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MO
FILE REFERENCE: PD-1010 CIP
CURRENT APPLICATION NUMBER: US/09/534,840
CURRENT FILING DATE: 1992-07-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 13675
SOFTWARE: PERL Program
SEQ ID NO 10418
LENGTH: 180
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01316725
NAME/KEY: unsure
LOCATION: 2-3
OTHER INFORMATION: a, t, c, g, or other
US-09-534-840-10418

Query Match 100.0%; Score 21; DB 20; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctggcgagcttggggcct 21
|||||
Db 73 GCTGGCGGAGTTGGGGCCT 53

RESULT 8
US-09-534-840-10431/c
; Sequence 10431, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLEC
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10431
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: hu01005556
US-09-534-840-10431

Query Match 100.0%; Score 21; DB 20; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctggcgagcttggggcct 21
|||||
Db 126 GCTGGCGGAGTTGGGGCCT 106

RESULT 9
US-09-534-840-10433/c
; Sequence 10433, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MOLEC
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10433
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: hu01233159
US-09-534-840-10433

Query Match 100.0%; Score 21; DB 20; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctggcgagcttggggcct 21
|||||
Db 134 GCTGGCGGAGTTGGGGCCT 114

RESULT 10
US-09-534-840-10383/c
; Sequence 10383, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MO
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10383
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: hu01273608
US-09-534-840-10383

Query Match 100.0%; Score 21; DB 20; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctggcgagcttggggcct 21
|||||
Db 132 GCTGGCGGAGTTGGGGCCT 112

RESULT 11
US-09-534-840-10419/c
; Sequence 10419, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING PROTEIN MODIFICATION MO
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10419
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: hu01048852
US-09-534-840-10419

Query Match 100.0%; Score 21; DB 20; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgagagttggggcct 21
|||||
Db 132 GCTGGCGGAGTTGGGGCCT 112

RESULT 12
US-09-534-840-10817/c
; Sequence 10817, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Sellhammer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10817
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01273243
US-09-534-840-10817

Query Match 100.0%; Score 21; DB 20; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgagagttggggcct 21
|||||
Db 134 GCTGGCGGAGTTGGGGCCT 114

RESULT 13
US-09-534-840-10368/c
; Sequence 10368, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Sellhammer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10368
; LENGTH: 254
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01255852
US-09-534-840-10368

Query Match 100.0%; Score 21; DB 20; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgagagttggggcct 21
|||||
Db 147 GCTGGCGGAGTTGGGGCCT 127

RESULT 14
US-09-534-840-10355/c
; Sequence 10355, Application US/09534840
; GENERAL INFORMATION:
; APPLICANT: Sellhammer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; FILE REFERENCE: PD-1010 CIP
; CURRENT APPLICATION NUMBER: US/09/534,840
; CURRENT FILING DATE: 1992-07-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13675
; SOFTWARE: PERL Program
; SEQ ID NO 10355
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01203156
; LOCATION: 26, 82, 92
; OTHER INFORMATION: a, t, c, g, or other
US-09-534-840-10355

Query Match 100.0%; Score 21; DB 20; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcgagagttggggcct 21
|||||
Db 183 GCTGGCGGAGTTGGGGCCT 163

RESULT 15
US-09-652-125A-330/c
; Sequence 330, Application US/09652125A
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600,1189-001
; CURRENT APPLICATION NUMBER: US/09/652,125A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/151,127
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 9506
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 330
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(261)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-125A-330

Query Match 100.0%; Score 21; DB 25; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctggcgcgagctgggggccc 21
|||||
Db 191 GCTGGCGCGAGCTGGGGGCT 171

Search completed: May 17, 2002, 17:56:01
Job time: 12668 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:06:12 ; Search time 111.1 seconds
(without alignments)

46,429 Million cell updates/sec

Title: US-09-913-325-12

Sequence: 1 gctggcgaggttggggccct 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/prodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCTUS.COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	16.8	80.0	3562	4	US-09-360-197-1
C 2	16.8	80.0	3647	4	US-09-360-197-7
C 3	16.4	78.1	50	1	US-08-171-389-590
C 4	16.4	78.1	50	1	US-08-123-936-590
C 5	16.4	78.1	50	2	US-08-475-228A-590
C 6	16.4	78.1	50	3	US-08-482-080A-590
C 7	16.4	78.1	50	3	PCT-US93-12388-590
C 8	16.4	78.1	68	2	US-08-790-963-66
C 9	16.4	78.1	68	4	US-09-371-774-66
C 10	16.4	78.1	256	3	US-09-106-182-24
C 11	16.4	78.1	256	4	US-09-227-357-10
C 12	16.4	78.1	271	3	US-09-106-182-18
C 13	16.4	78.1	271	4	US-09-227-357-5
C 14	16.4	78.1	356	3	US-08-945-726-1
C 15	16.4	78.1	372	1	US-08-822-962-1
C 16	16.4	78.1	600	1	PCT-US91-02766-23
C 17	16.4	78.1	600	6	5219759-5
C 18	16.4	78.1	633	1	US-08-644-664B-6
C 19	16.4	78.1	633	2	US-08-761-277A-6
C 20	16.4	78.1	634	4	US-09-308-160B-25
C 21	16.4	78.1	664	1	US-08-455-755-1
C 22	16.4	78.1	664	2	US-07-910-260-1
C 23	16.4	78.1	664	5	PCT-US91-00878-1
C 24	16.4	78.1	2037	1	US-08-143-497-4
C 25	16.4	78.1	2037	1	US-08-461-666-4
C 26	16.4	78.1	2037	1	US-08-461-184-4
C 27	16.4	78.1	2037	1	US-08-463-675-4

ALIGNMENTS

C 28	16.4	78.1	2037	1	US-08-757-300-4	Sequence 4, Appl1
C 29	16.4	78.1	2037	1	US-08-464-589-4	Sequence 4, Appl1
C 30	16.4	78.1	2800	3	US-08-869-841B-42	Sequence 42, Appl1
C 31	16.4	78.1	3390	4	US-08-993-088A-5	Sequence 5, Appl1
C 32	16.4	78.1	3390	4	US-08-993-424B-5	Sequence 5, Appl1
C 33	16.4	78.1	3705	3	US-09-282-996-3	Sequence 3, Appl1
C 34	16.4	78.1	3944	1	US-07-678-408A-1	Sequence 1, Appl1
C 35	16.4	78.1	4059	2	US-08-252-493C-4	Sequence 4, Appl1
C 36	16.4	78.1	4059	3	US-09-276-197-4	Sequence 4, Appl1
C 37	16.4	78.1	4059	4	US-08-487-283A-3	Sequence 3, Appl1
C 38	16.4	78.1	4059	5	PCT-US95-07354-4	Sequence 4, Appl1
C 39	16.4	78.1	4059	5	PCT-US96-05611A-11	Sequence 11, Appl1
C 40	16.4	78.1	4454	1	US-07-712-284-1	Sequence 1, Appl1
C 41	16.4	78.1	4454	5	PCT-US92-04227-1	Sequence 7, Appl1
C 42	16.4	78.1	4665	3	US-08-948-378A-7	Sequence 7, Appl1
C 43	16.4	78.1	4665	4	US-09-169-425C-7	Sequence 7, Appl1
C 44	16.4	78.1	4696	2	US-08-929-967-15	Sequence 15, Appl1
C 45	16.4	78.1	4732	1	US-07-884-811-1	Sequence 1, Appl1

RESULT 1
US-09-360-197-1/c
; Sequence 1, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassiliana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Dewelle, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FIDE REFERENCE: 989, 6706P
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: US/09/360,197
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ. ID NOS: 22
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3562
; TYPE: DNA
; ORGANISM: ratlus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)..(1700)
US-09-360-197-1
Query Match 80.0%; Score 16.8; DB 4; Length 3562;
Best local similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1778 gctggcgaggttggggcc 1759
Oy 1 gctggcgaggttggggcc 20
Db 1778 gctggcgaggttggggcc 1759
RESULT 2
US-09-360-197-7/c
; Sequence 7, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassiliana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Dewelle, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications

FILE REFERENCE: 989.6706P
CURRENT APPLICATION NUMBER: US/09/360.197
CURRENT FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: 09/129.758
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: 60/095.408
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 7
LENGTH: 3647
TYPE: DNA
ORGANISM: rattus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (109)..(1785)
US-09-360-197-7

Query Match 80.0%; Score 16.8; DB 4; Length 3647;
Best Local Similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gctgggcgagctgggggccc 20
||||| |
Db 1863 GCTGGGGCAGCTTGGGGGCC 1844

RESULT 3
US-08-171-389-590/C
Sequence 590, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171.389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123.936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996.783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723.618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081.070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-08-171-389-590

Query Match 78.1%; Score 16.4; DB 1; Length 50;
Best Local Similarity 94.4%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgggcgagctggggccc 19
||||| |
Db 20 CTGGCGCAGCTTAGCGGC 3

RESULT 4
US-08-123-936-590/C
Sequence 590, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123.936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996.783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723.618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE: NO
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-08-123-936-590

Query Match 78.1%; Score 16.4; DB 1; Length 50;
Best Local Similarity 94.4%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctggcgagattg99g9c 19
|||||
DB 20 CTGGCGGAGATTAGGGGC 3

RESULT 5
US-08-475-228A-590/c
Sequence 590, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475, 228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123, 936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996, 783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723, 618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081, 070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-08-475-228A-590

Query Match 78.1%; Score 16.4; DB 2; Length 50;
Best Local Similarity 94.4%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctggcgagattg99g9c 19
|||||
DB 20 CTGGCGGAGATTAGGGGC 3

RESULT 6
US-08-482-080A-590/c
Sequence 590, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482, 080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171, 389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123, 936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996, 783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723, 618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081, 070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-08-482-080A-590

Query Match 78.1%; Score 16.4; DB 3; Length 50;
Best Local Similarity 94.4%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 ctggcgaggttgaggc 19
|||||
DB 20 CTGGCGGAGTTAGGGC 3

RESULT 7
PCT-US93-12388-590/C
Sequence 590, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
PCT-US93-12388-590

Query Match 78.1%; Score 16.4; DB 5; Length 50;
Best Local Similarity 94.4%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 ctggcgaggttgaggc 19
|||||
DB 20 CTGGCGGAGTTAGGGC 3

RESULT 8
US-08-790-963-66
Sequence 66, Application US/08790963
Patent No. 5837464
GENERAL INFORMATION:
APPLICANT: Daniel J. Capon
ADDRESSEE: Christos John Petropoulos
TITLE OF INVENTION: Compositions and Methods For
TITLE OF INVENTION: Determining Anti-viral Drug Susceptibility And
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,963
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50130-B/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-790-963-66

Query Match 78.1%; Score 16.4; DB 2; Length 68;
Best Local Similarity 94.4%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 ctggcgaggttgaggc 19
|||||
DB 33 CTGGCGGAGTTAGGGC 50

RESULT 9
US-09-371-774-66
Sequence 66, Application US/09371774
Patent No. 6242187
GENERAL INFORMATION:
APPLICANT: Daniel J. Capon
ADDRESSEE: Christos John Petropoulos
TITLE OF INVENTION: Compositions and Methods For
TITLE OF INVENTION: Determining Anti-viral Drug Susceptibility And
TITLE OF INVENTION: Resistance and Anti-viral Drug Screening
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/371,774
FILING DATE: 10-Aug-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50130-F/JPM/CMR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-371-774-66

Query Match 78.1%; Score 16.4; DB 4; Length 68;
Best Local Similarity 94.4%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctggcgagattggggc 19
|||||
Db 33 CTGGCGGAGATTGAGGCG 50

RESULT 10
US-09-106-182-24/c
Sequence 24, Application US/09106182
Patent No. 6046035
GENERAL INFORMATION:
APPLICANT: Shi, Yangu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-106-182-24

Query Match 78.1%; Score 16.4; DB 3; Length 256;
Best Local Similarity 94.4%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctggcgagattggggc 19
|||||
Db 123 CTGGCGGAGATTGAGGCG 106

RESULT 11
US-09-227-357-10/c
Sequence 10, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947

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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-357-10

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Query Match      78.1%  Score 16.4;  DB 4;  Length 256;
Best Local Similarity 94.4%;  Pred. No. 90;
Matches 17;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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QY      2  cctggcgagagttg99g9c 19
          |||||
Db      123  CTGGCGGAGATTAGGCGC 106

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```

RESULT 12
US-09-106-182-18/c
; Sequence 18, Application US/09106182
; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,182
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/051,053
; FILING DATE: 30-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 18:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-106-182-18

```

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Query Match      78.1%  Score 16.4;  DB 3;  Length 271;
Best Local Similarity 94.4%;  Pred. No. 90;
Matches 17;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

QY      2  cctggcgagagttg99g9c 19
          |||||
Db      138  CTGGCGGAGATTAGGCGC 121

```

```

RESULT 13
US-09-227-357-5/c
; Sequence 5, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010p1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950

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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055, 947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055, 964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056, 360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055, 684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055, 984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055, 954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058, 785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058, 664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058, 660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058, 661
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058, 661
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-357-5
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Query Match          78.1%; Score 16.4; DB 4; Length 271;
Best Local Similarity 94.4%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Oy 2 ctggcgagattgggggc 19
    |||||||
Db 138 CTGGCGGAGTTAGGGGC 121
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```
RESULT 14
US-08-945-726-1/C
; Sequence 1, Application US/08945726
; Patent No. 6004813
; GENERAL INFORMATION:
; APPLICANT: SERLUP-I-CRESCENZI, Ottaviano
; APPLICANT: PEZZOTTI, Annarita
; TITLE OF INVENTION: IL-6 ACTIVITY INHIBITORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945, 726
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25, 618
; REFERENCE/DOCKET NUMBER: SERLUP-I-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 356 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-945-726-1
```

```
Query Match          78.1%; Score 16.4; DB 3; Length 356;
Best Local Similarity 94.4%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy 2 ctggcgagattgggggc 19
    |||||||
Db 223 CTGGCGGAGTTAGGGGC 206
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RESULT 15
US-08-822-982-1
; Sequence 1, Application US/08822982
; Patent No. 5827705
; GENERAL INFORMATION:
; APPLICANT: Dean, David A.
; TITLE OF INVENTION: MOLECULE AND METHOD FOR IMPORTING DNA
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822, 982
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013, 863
; FILING DATE: 22-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032, 468
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BRAMAN, SUSAN J.
; REGISTRATION NUMBER: 34, 103
; REFERENCE/DOCKET NUMBER: 21467/32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1600
; TELEFAX: 716-263-1636
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-822-982-1
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Query Match          78.1%; Score 16.4; DB 1; Length 372;
Best Local Similarity 94.4%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 ctggcgagattgggggc 19
    |||||||
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Mon May 20 10:17:49 2002

us-09-913-325-12.rni

Page 8

Db 134 CTGGCGGAGTTAGGGC 151

Search completed: May 17, 2002, 16:06:13
Job time: 12747 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:13:55 ; Search time 447.74 Seconds
(without alignments)
80.527 Million cell updates/sec

Title: US-09-913-325-12

Perfect score: 21

Sequence: 1 gctggcgaggttggggcct 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	AAA94234	Human testostosterone
2	21	100.0	975	AAZ41353	Human normal uterus
3	21	100.0	1512	ABA83111	Apolipoprotein J
4	21	100.0	1678	AAH23086	Osteoarthritis tis
5	21	100.0	2876	AAAC90467	Human uncoupling p
6	16.8	80.0	2535	AAH25134	Nucleotide sequenc
7	16.8	80.0	2962	AAH28161	Rat acid sensitive
8	16.8	80.0	3562	AAV60839	Rat acid sensing i
9	16.8	80.0	3562	AAZ61197	CDNA encoding a ra

C 10	16.8	80.0	3647	19	AAV60842	Rat acid sensing i
C 11	16.8	80.0	3647	21	AAZ61200	CDNA encoding a ra
C 12	16.8	80.0	4121	21	AACT5317	Human ORFX ORF872
C 13	16.8	80.0	14654	22	AAH28620	Genomic sequence #
C 14	16.4	78.1	50	15	AAO63840	Simian virus 40 T/
C 15	16.4	78.1	50	18	AAH64302	SV40 T/ Late (sta
C 16	16.4	78.1	50	20	AAH17590	Test sequence from
C 17	16.4	78.1	68	20	AAV64746	HIV anti-viral oli
C 18	16.4	78.1	68	22	AAH24758	Nucleotide sequenc
C 19	16.4	78.1	185	10	AAH90660	Sequence of SV40 e
C 20	16.4	78.1	204	21	AAH12021	Murine lactate deh
C 21	16.4	78.1	223	21	AAH12017	Human enolase A pr
C 22	16.4	78.1	231	21	AACT3859	SV40 promoter sequ
C 23	16.4	78.1	237	21	AAH12001	Murine PGK HRE der
C 24	16.4	78.1	242	20	AAH207789	Promoter Obhel1 us
C 25	16.4	78.1	242	21	AAH12016	Murine PGK HRE der
C 26	16.4	78.1	243	20	AAH11397	Murine PGK HRE der
C 27	16.4	78.1	243	21	AAH11995	Murine PGK HRE der
C 28	16.4	78.1	252	19	AAV52535	Sequence of SV40 e
C 29	16.4	78.1	256	19	AAV34153	Nuclear factor kap
C 30	16.4	78.1	256	19	AAV35910	Nuclear factor kap
C 31	16.4	78.1	256	19	AAV34285	Nuclear factor kap
C 32	16.4	78.1	256	19	AAV65610	Nuclear factor kap
C 33	16.4	78.1	256	20	AAH19858	Nuclear factor RB-
C 34	16.4	78.1	256	20	AAH24810	Chimeric NF-kB bin
C 35	16.4	78.1	256	20	AAH209783	NF-kappaB/SV40 ear
C 36	16.4	78.1	256	20	AAH210684	Nucleotide sequenc
C 37	16.4	78.1	256	20	AAH200409	SV40 promoter temp
C 38	16.4	78.1	256	20	AAH200801	SV40 early promote
C 39	16.4	78.1	256	20	AAH206218	SV40 promoter cont
C 40	16.4	78.1	256	20	AAH297915	Nuclear factor cont
C 41	16.4	78.1	256	20	AAH297910	Nuclear factor kap
C 42	16.4	78.1	256	20	AAH28675	Nucleotide sequenc
C 43	16.4	78.1	256	20	AAH28675	SV40 promoter cont
C 44	16.4	78.1	256	20	AAH35900	NF-kappa B promote
C 45	16.4	78.1	256	20	AAH37368	Human NF-kappaB pr

ALIGNMENTS

RESULT 1	AAA94234	standard; DNA: 21 BP.
ID	AAA94234	
XX	AAA94234:	
AC	12-JAN-2001 (first entry)	
DT		
XX	Human testostosterone-repressed prostate message-2 antisense oligo #10.	
DE		
XX	Human: testostosterone-repressed prostate message-2; TRPM-2; clusterin;	
KW	sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200049937-A2.	
PD	31-AUG-2000.	
XX		
PF	25-FEB-2000; 2000WO-US04875.	
XX		
XX	26-FEB-1999; 99US-0121726.	
PR		
XX		
PA	(UYBR-) UNIV BRITISH COLUMBIA.	
XX		
PI	Gleave M, Rennie PS, Miyake H, Nelson C;	
XX	WPI; 2000-533132/48.	
DR		
XX	Treating prostatic tumors and renal cancers by antisense inhibition of	
PT	the testosterone-repressed prostate messenger-2 gene -	
XX		

PS Example 5: Page 38; 38pp; English.
XX
CC The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2), also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed
CC at human TRPM-2 can be used in the treatment of tumour cells expressing
CC the TRPM-2 gene. These include prostate cancer, renal cell cancer and
CC some breast cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective.
XX
SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gctggcgaggtggggcct 21
|||||
Db 1 gctggcgaggtggggcct 21

RESULT 2
AAZ1353/C
ID AAZ1353 standard; CDNA: 975 BP.
XX
AC AAZ1353;
XX
XX 19-JAN-2000 (first entry)
XX
DE Human normal uterus tissue derived CDNA 29.
XX
KW Human: uterus; cancer; treatment; anticancer; cytostatic; gene therapy;
KW EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
OS
XX
PN DE19817946-A1.
XX
PD 21-OCT-1999.
XX
PF 17-APR-1998; 98DE-1017946.
XX
PR 17-APR-1998; 98DE-1017946.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
XX
DR WPI: 1999-591956/51.
XX
XX New nucleic acid sequences expressed in normal uterine tissues, and
PT derived polypeptides, for treatment of uterine cancer and
PT identification of therapeutic agents -
XX
PS Claim 3; Page 95; 154pp; German.
XX
CC This invention describes novel CDNA sequences (A) highly expressed in
CC normal uterine tissue which can have anticancer and cytostatic activity
CC and can be used for gene therapy. (A) are used (i) for recombinant
CC expression of polypeptides (B) and (ii) to isolate complete genes.
CC (B) are used (i) to identify agents suitable for treatment of uterine
CC cancer; (ii) directly for treating this form of cancer (including
CC expression from gene therapy vectors) and (iii) for generation of
CC specific antibodies. (A) are identified by assembling ESTs (expressed
CC sequence tags) from a particular tissue type before comparison of
CC expression patterns. This allows a significantly longer fragment of the
CC gene to be revealed, so should reduce the number of failures associated
CC with the fact that ESTs from different libraries may represent
CC different parts of the same unknown gene, distorting the estimated
CC frequency of occurrence in a particular tissue. AAZ1325-241385

CC represent the human uterine tissue derived CDNA fragments of the
CC invention which encode the protein fragments represented in
CC AAY9838-Y59892.
XX
SQ Sequence 975 BP; 221 A; 320 C; 248 G; 186 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 975;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gctggcgaggtggggcct 21
|||||
Db 903 gctggcgaggtggggcct 883

RESULT 3
ABA83111/C
ID ABA83111 standard; DNA: 1512 BP.
XX
AC ABA83111;
XX
XX 08-FEB-2002 (first entry)
XX
DE Apolipoprotein J ovarian tumour marker gene, SEQ ID NO:59.
XX
XX Ovarian tumour marker gene; human; overexpression; upregulation;
KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
KW identification; serous cystadenoma; borderline serous tumour;
KW mucinous cystadenocarcinoma; mucinous cystadenocarcinoma;
KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
KW immune response pathway; cell proliferation regulation; protein folding;
KW membrane localized; secreted; therapeutic target; cytostatic;
KW gene therapy; vaccine; ds.
XX
XX Homo sapiens.
XX
OS
XX
PN WO200175177-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10947.
XX
PR 03-APR-2000; 2000US-194336P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
XX
XX WPI: 2001-626450/72.
XX
DR P-PSDB: ABB50285.
XX
XX Detecting and identifying ovarian tumor, identifying increased risk for
PT developing ovarian cancer, and determining effectiveness of ovarian
PT cancer treatment, by measuring expression level of ovarian tumor marker
PT gene -
XX
PS Claim 23; Page 103; 140pp; English.
XX
XX The invention relates to methods for diagnosing and prognosing ovarian
CC tumours in an individual via the detection and measurement of the
CC expression of ovarian tumor marker genes (ABA83081-ABA83122, ABA83180,
CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83159, ABA83179,
CC ABA83181 and ABA83183). The methods of the invention are useful for
CC detecting an ovarian tumor in a patient, for identifying an individual
CC at increased risk for developing ovarian cancer, in prognostic tests for
CC assessing the relative severity of ovarian cancer, in tests for
CC monitoring a patient in remission from ovarian cancer and in tests for
CC monitoring disease status in a patient being treated for ovarian cancer.
CC The methods can additionally be used to identify a particular tumour as
CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from

CC disease-modifying activity of osteoarthritis drugs. Other disorders
 CC treatable using the nucleic acid sequences include atopic, inflammatory
 CC and infectious disorders e.g. Crohn's disease and sepsis, and wound
 CC healing.
 XX
 SQ Sequence 1678 BP; 424 A; 491 C; 450 G; 313 T; 0 other;
 50
 Query Match 100.0%; Score 21; DB 22; Length 1678;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 gctggcgcgagttggtggcct 21
 ||||||||||||||||
 Db 1558 gctggcgcgagttggtggcct 1538
 RESULT 5
 AAC90467/c
 ID AAC90467 standard; cDNA: 2876 BP.
 XX
 AC AAC90467;
 XX
 DT 12-MAR-2001 (first entry)
 XX
 DE Human uncoupling protein cDNA #16.
 XX
 KW Human; uncoupling protein; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cardiant; vasotropic;
 KW cerebroprotective; neuroprotective, antibacterial; ophthalmological;
 KW gastrointestinal; nephrotropic; gynaecological; vulnery; thrombolytic;
 KW gene therapy; cancer; wound; infectious disease; thrombosis; arthritis.
 KW Interfility; ss.
 XX
 KW Homo sapiens.
 OS
 XX
 XX W0200061614-A2.
 PV
 XX 19-OCT-2000.
 PD
 XX
 XX 06-APR-2000; 2000WO-US09534.
 PF
 XX
 XX 09-APR-1999; 99US-0128701.
 PR 08-JUL-1999; 99US-0142821.
 PR 18-AUG-1999; 99US-0149448.
 PR 12-NOV-1999; 99US-0164751.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, NI J, Komatsoulis G, Rosen CA, Soppet DR;
 PI
 XX
 DR WPI: 2000-656322/63.
 DR P-PSDB: AAB50393.
 XX
 XX
 PT uncoupling proteins and nucleic acid sequences encoding them, useful
 for detecting, preventing and treating proliferative, neurological,
 immune system, cardiovascular and gastrointestinal disorders -
 XX
 Claim 1; Page 313-314; 343pp; English.
 PS
 XX
 XX The present sequence is one of eighteen isolated nucleotide sequences
 CC encoding uncoupling proteins. The nucleotide sequences may be used for
 CC the detection of various disorders such as cancer, for chromosome
 CC identification, as chromosome markers and for numerous other diagnostic
 CC or research purposes. The uncoupling protein encoded by the nucleotide
 CC sequences may be used to treat disorders such as neural, immune,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal and proliferative disorders, wounds, infectious diseases,
 CC thrombosis, arthritis, and interfility.
 CC
 SQ Sequence 2876 BP; 775 A; 695 C; 669 G; 737 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 2876;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gctggcgagcttggggcct 21
|||||
DB 2734 GCTGGCGGAGTTGGGGCCT 2714

RESULT 6
AAH25134/C
ID AAH25134 standard; DNA: 2535 BP.
XX
AC AAH25134;
XX
DT 22-AUG-2001 (first entry)
XX
DE Nucleotide sequence of human alcohol dehydrogenase 21612.
XX
KM Human: alcohol dehydrogenase; colon disorder; brain disorder;
KM skin disorder; heart disorder; blood vessel disorder; kidney disorder;
KM prostate disorder; skeletal muscle disorder; ovary disorder;
KM testis disorder; epididymis disorder; spleen disorder; lung disorder;
KM liver disorder; uterus disorder; endometrium disorder; T-cell disorder;
KM red cell disorder; thymus disorder; B cell disorder; breast disorder;
KM thyroid disorder; pancreas disorder; small intestine disorder;
KM reduced platelet number disorder; precursor T cell neoplasm; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 762..2018
FT /tag= a
FT /product= "alcohol dehydrogenase 21612"
XX
PN WO20014446-A2.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-US33873.
XX
PR 15-DEC-1999; 99US-0464039.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers R;
XX
PI WPI: 2001-390244/41.
XX
DR P-PSDB: AAB84367.
XX
PT Novel human alcohol dehydrogenase proteins; 21612, 21615, 21620, 21676,
PT 33756, useful for treating psoriasis, tropical sprue, pancreatitis,
PT golfer, osteomalacia, endometriosis, angina pectoris, embolism
XX
PS Claim 2; Fig 15; 156pp; English.
XX
CC AAH25131-35 encode human alcohol dehydrogenase proteins, designated
CC 21620, 33756, 21676, 21612 and 21615, respectively. Alcohol dehydrogenase
CC polynucleotides and polypeptides are useful for treatment and diagnosis
CC of disorders mediated by or related to alcohol dehydrogenase. They can
CC be used for treating disorders of colon, brain, skin, heart, blood
CC vessels, kidney, prostate, skeletal muscle, ovary, testis and epididymis,
CC spleen, lung, liver, uterus and endometrium, T-cells, red cells, thymus,
CC B cells, breast, thyroid, pancreas, small intestine, reduced platelet
CC number, precursor T cell neoplasms, bone forming cells, and bone marrow
CC cells.
XX
SQ Sequence 2535 BP; 720 A; 531 C; 537 G; 695 T; 52 other;

Query Match 80.0%; Score 16.8; DB 22; Length 2535;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gctggcgagcttggggcct 20
|||||
DB 73 GATGGCGGAGTTAGGGGCC 54

RESULT 7
AAH28161/C
ID AAH28161 standard; cDNA to mRNA; 2962 BP.
XX
AC AAH28161;
XX
DT 16-JUN-1999 (first entry)
XX
DE Rat Acid sensitive ion channel coding sequence.
XX
KM Acid sensitive ion channel; rat; ASIC; pH mediated pain disorder;
KM ischemia; gene therapy; proton-gated ion channel; ds.
XX
OS Rattus sp.
XX
PN WO9911784-A1.
XX
PD 11-MAR-1999.
XX
PF 28-AUG-1998; 98WO-GB02609.
XX
PR 29-AUG-1997; 97GB-0018365.
XX
PA (UNIO) UNIV COLLEGE LONDON.
XX
PI Akopian AN, Chen C, England S, Wood JN;
XX
PI WPI: 1999-205188/17.
XX
DR P-PSDB: AAY03186.
XX
PT Acid sensitive ion channel (ASIC) proteins - useful in gene therapy
PT for treatment of pH mediated pain disorders
XX
PS Claim 7; Page 43-47; 62pp; English.
XX
CC This sequence encodes an acid sensitive ion channel (ASIC) of the
CC invention, isolated from rat dorsal root ganglion. Antisense ASIC DNA or
CC RNA is useful in gene therapy for downgrading expression of ASIC protein,
CC for pH mediated pain disorders e.g. in ischemia. The vectors are useful
CC for incorporating ASIC DNA or RNA for use in gene therapy. Proton-gated
CC ion channel agonists and antagonists are identified using cells
CC transformed with ASIC DNA by allowing interaction between the candidate
CC substance and ASIC protein in the membrane, and measuring interaction
CC and/or cell response. Partial agonists and antagonists can be identified
CC by their ability to block the response of the cell to present in a
CC solution of a given acid pH or any agonist. The hybridisation probes are
CC useful for screening libraries for ASIC DNA or RNA.
XX
SQ Sequence 2962 BP; 655 A; 850 C; 785 G; 672 T; 0 other;

Query Match 80.0%; Score 16.8; DB 20; Length 2962;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 gctggcgagcttggggcct 20
|||||
DB 1824 GCTGGCGGAGTTAGGGGCC 1805

RESULT 8
AAV60839/C
ID AAV60839 standard; DNA; 3562 BP.
XX
AC AAV60839;
XX
DT 02-FEB-1999 (first entry)

XX Rat acid sensing ionic channel ASIC1A gene.

DE Rat; neuronal cationic channel; amiloride; proton; ASIC; brain; probe;
XX acid sensing ionic channel; hybridisation; primer; PCR; amplification;
KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;
KW tumour; cerebral neurodegeneration; transgenic animal; knockout animal;
KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;
KW amyotrophic lateral sclerosis; cerebellar ataxia; ds.

OS Rattus sp.

XX Key Location/Qualifiers
FH 123..1703
FT CDS /tag= a
FT /product= "ASIC1A"
FT /note= "acid sensing ionic channel 1A"

XX MO9835034-A1.

XX 13-AUG-1998.

XX 11-FEB-1998; 98WO-FR00270.

XX 28-JUL-1997; 97FR-0009587.

XX 11-FEB-1997; 97FR-0001574.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Bassilana F, Champigny G, Heurteaux C, Lazdunski M;
PI Waldmann R, Lingueglia E;

XX WPI: 1998-447231/38.

XX P-PSDB; AAW68504.

XX Protein comprising proton-sensitive neuronal channel - useful for
PT screening for analgesics and for treating neurodegeneration

XX Claim 12; Page 24-27; 64pp; French.

XX This sequence represents the gene encoding a rat neuronal cationic
XX channel that is sensitive to amiloride and activated by protons and
XX is designated Acid Sensing Ionic Channel (ASIC). This sequence
XX represents the rat ASIC1A gene. The sequence was isolated from a rat
XX brain DNA library using a probe amplified by primers AAV60845-V60846.
XX The protein can be used to screen for modulators of these channels,
XX particularly to identify compounds that modulate perception of acidity,
XX as regards nociception (pain) rather than taste. These compounds are
XX used to treat or prevent pain associated with acidity (e.g. in cases of
XX inflammation, ischaemia or some tumours) and as inhibitors of
XX neurodegeneration caused by overexpression of the channels. Antibodies
XX to the protein are used to detect the channels in tissues, and to act
XX therapeutically as channel modulators. The nucleic acid can be used to
XX generate transgenic, particularly knockout, animals for studying
XX ASIC-related disorders, also for gene therapy. The channel protein,
XX or its (anti)agonists, can be used to treat or prevent cerebral
XX neurodegenerative conditions (e.g. Alzheimer's, Parkinson's or
XX Huntington's diseases, amyotrophic lateral sclerosis or cerebellar
XX ataxia.

XX Sequence 3562 BP; 905 A; 827 C; 862 G; 968 T; 0 other;

XX Query Match

XX Best Local Similarity 80.0%; Score 16.8; DB 19; Length 3562;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 1 gctggcgagcttggggcc 20

DB 1778 GCTGGGCGCAGTTGGGGCC 1759

RESULT 9

AAZ61197/c
ID AAZ61197 standard; cDNA; 3562 BP.

XX AAZ61197;

XX 30-MAY-2000 (first entry)

XX cDNA encoding a rat acid-sensitive cationic channel 1A (rASIC1A).

XX Neuronal acid-sensitive cation channel; ASIC; ASIC 1A;

XX proton-gated cation channel; biphasic desensitisation; amiloride;
KW cation transport channel; acid sensor; pH detection; ds.

OS Rattus sp.

XX Key Location/Qualifiers
FH 123..1703
FT CDS /tag= a
FT /product= "acid-sensitive cationic channel 1A"

XX WO200008149-A2.

XX 17-FEB-2000.

XX 05-AUG-1999; 99WO-IB01445.

XX 05-AUG-1998; 98US-0095408.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Waldmann R, Bassilana F, Lazdunski M, De Weille JR;

XX WPI: 2000-195574/17.

XX P-PSDB; AAV69175.

XX Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
PT to identify substances capable of modulating cation transport channel
PT activity -

XX Disclosure; Page 63-66; 84pp; English.

XX The present sequence encodes a rat neuronal acid-sensitive cation
XX channel 1A (ASIC1A) protein. The protein is a proton-gated cation
XX channel subunit that has biphasic desensitisation kinetics with both
XX a rapidly inactivating sodium-selective and a sustained component. The
XX channels are sensitive to amiloride. The specification describes ASIC3
XX proteins, which are expressed in the sensory neurons but not in the
XX brain. The cation transport channel proteins can be used in methods to
XX identify substances capable of modulating the activity of cation
XX transport channels. The human ASIC3 protein is also an acid sensor,
XX and might play an important role in the detection of lasting pH changes
XX in humans.

XX Sequence 3562 BP; 905 A; 827 C; 862 G; 968 T; 0 other;

XX Query Match

XX Best Local Similarity 80.0%; Score 16.8; DB 21; Length 3562;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 1 gctggcgagcttggggcc 20

DB 1778 GCTGGGCGCAGTTGGGGCC 1759

XX RESULT 10

XX AAV60842/c

XX AAV60842;

XX 02-FEB-1999 (first entry)

DE Rat acid sensing ionic channel ASIC1B gene.

KW Rat: neuronal cationic channel; amiloride; proton; ASIC; brain; probe;
 KW acid sensing ionic channel; hybridisation; primer; PCR; amplification;
 KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;
 KW tumour; cerebral neurodegeneration; transgenic animal; knockout animal;
 KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;
 KW amyotrophic lateral sclerosis; cerebellar ataxia; ds.

XX Rattus sp.

OS Rattus sp.
 FH Key Location/Qualifiers
 FT CDS 109..1788
 FT /tag= a
 FT /product= "ASIC1B"
 FT /note= "acid sensing ionic channel 1B"

XX WO9835034-A1.

XX 13-AUG-1998.

XX 11-FEB-1998; 98WO-FR00270.

XX 28-JUL-1997; 97FR-0009587.
 XX 11-FEB-1997; 97FR-0001574.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Bassilana F, Champigny G, Heurteaux C, Lazdunski M;
 PI Waldmann R, Lingueglia E;

XX WPI; 1998-447231/38.

DR P-PSDB; AAM68507.

PT Protein comprising proton-sensitive neuronal channel - useful for
 PT screening for analgesics and for treating neurodegeneration

XX Claim 15: Page 34-37; 64pp; French.

XX This sequence represents the gene encoding a rat neuronal cationic
 CC channel that is sensitive to amiloride and activated by protons and
 CC is designated Acid Sensing Ionic Channel (ASIC). This sequence
 CC represents the rat ASIC1B gene. The protein can be used to screen for
 CC modulators of these channels, particularly to identify compounds that
 CC modulate perception of acidity, as regards nociception (pain) rather than
 CC taste. These compounds are used to treat or prevent pain associated with
 CC acidity (e.g. in cases of inflammation, ischaemia or some tumours) and as
 CC inhibitors of neurodegeneration caused by overexpression of the channels.
 CC Antibodies to the protein are used to detect the channels in tissues, and
 CC to act therapeutically as channel modulators. The nucleic acid can be
 CC used to generate transgenic, particularly knockout, animals for studying
 CC ASIC-related disorders, also for gene therapy. The channel protein,
 CC or its (ant)agonists, can be used to treat or prevent cerebral
 CC neurodegenerative conditions (e.g. Alzheimer's, Parkinson's or
 CC Huntington's diseases, amyotrophic lateral sclerosis or cerebellar
 CC ataxia).

XX Sequence 3647 BP; 895 A; 853 C; 900 G; 999 T; 0 other;

Query Match 80.0%; Score 16.8; DB 19; Length 3647;
 Best Local Similarity 90.0%; Pred. No. 4.1e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gctggcgaggttg99ggcc 20
 ||||| |
 DB 1863 GCTGGGCGCAGTTGGGGGCC 1844

RESULT 11
 AA261200/c
 ID AA261200 standard; CDNA; 3647 BP.
 XX

AC AA261200;

XX 30-MAY-2000 (first entry)

XX cDNA encoding a rat acid-sensitive cationic channel 1B (rASIC1B).

XX Neuronal acid-sensitive cation channel; ASIC; ASIC 1B;
 KW proton-gated cation channel; biphasic desensitisation; amiloride;
 KW cation transport channel; acid sensor; pH detection; ds.

XX Rattus sp.

OS Rattus sp.
 FH Key Location/Qualifiers
 FT CDS 109..1788
 FT /tag= a
 FT /product= "acid-sensitive cationic channel 1B"

XX WO200008149-A2.

XX 17-FEB-2000.

XX 05-AUG-1999; 99WO-IB01445.

XX 05-AUG-1998; 98US-0095408.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Waldmann R, Bassilana F, Lazdunski M, De Weille JR;
 PI WPI; 2000-195574/17.
 DR P-PSDB; AAV69178.

PT Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
 PT to identify substances capable of modulating cation transport channel
 PT activity

XX Disclosure; Page 73-76; 84pp; English.

XX The present sequence encodes a rat neuronal acid-sensitive cation
 CC channel 1B (ASIC1B) protein. The protein is a proton-gated cation
 CC channel subunit that has biphasic desensitisation kinetics with both
 CC a rapidly inactivating sodium-selective and a sustained component. The
 CC channels are sensitive to amiloride. The specification describes ASIC3
 CC proteins, which are expressed in the sensory neurons but not in the
 CC brain. The cation transport channel proteins can be used in methods to
 CC identify substances capable of modulating the activity of cation
 CC transport channels. The human ASIC3 protein is also an acid sensor,
 CC and might play an important role in the detection of lasting pH changes
 CC in humans.

XX Sequence 3647 BP; 895 A; 853 C; 900 G; 999 T; 0 other;

Query Match 80.0%; Score 16.8; DB 21; Length 3647;
 Best Local Similarity 90.0%; Pred. No. 4.1e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gctggcgaggttg99ggcc 20
 ||||| |
 DB 1863 GCTGGGCGCAGTTGGGGGCC 1844

RESULT 12
 AAC75317
 ID AAC75317 standard; CDNA; 4121 BP.
 XX AAC75317;

XX 08-FEB-2001 (first entry)

XX Human ORFX ORF872 polynucleotide sequence SEQ ID NO:1743.
 XX Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
 KW

XX vulnereva; antiposlastic; antiparkinsonian; nootropic; neuroprotective;
KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
KM antiviral; antibacterial; antifungal; antihemmatic; antithyroid;
KM antineuic; gene therapy; cancer; proliferative disorder; hypertension;
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KM cholesterol ester storage; systemic lupus erythematosus; infection;
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KM allergy; aplastic anemia; nocturnal hemoglobinuria; burn; wound;
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
KM thrombosis; contraceptive; ss.
XX
XX Homo sapiens.
OS
XX WO200058473-A2.
XX
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000MO-US08621.
XX
XX 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
XX (CURA-) CURAGEN CORP.
PA
PI Shinkets RA, Leach M;
XX
XX WPI; 2000-602362/57.
DR P-PSDB: AAB41108.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 5; Page 1376-1378; 5507pp; English.
PS
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antiposlastic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antihemmatic;
CC antithyroid; and antineuic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal hemoglobinuria, antiinflammatory disease, to enhance
CC coagulation, to inhibit thrombosis, and as a contraceptive.
XX
XX Sequence 4121 BP; 818 A; 1186 C; 1260 G; 857 T; 0 other;
XX
XX Query Match 80.0%; Score 16.8; DB 21; Length 4121;
XX Best Local Similarity 90.0%; Pred. No. 4.1e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 ctggcgaggttgaggacct 21
XX ||| ||||| ||||| |||||
XX 2519 ctggcgaggttgaggacct 2538

RESULT	13
AA528620	
ID	AA528620 standard; DNA; 14654 BP.
XX	
AC	
XX	AA528620;
DT	07-NOV-2001 (first entry)
DE	Genomic sequence #460 encoding for novel human respiratory antigen.
XX	
KW	Human; respiratory antigen; respiratory disorder; throat disorder;
KW	lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
KW	anti allergic; anti asthmatic; anti inflammatory; olfactory;
KW	respiratory active; ds.
XX	
OS	Homo sapiens.
PN	W020015448-A1.
XX	
PD	02-AUG-2001.
XX	
EF	17-JAN-2001; 2001WO-US01333.
XX	
PR	31-JAN-2000; 2000US-0179065.
PR	04-FEB-2000; 2000US-0180628.
PR	24-FEB-2000; 2000US-0184664.
PR	02-MAR-2000; 2000US-0186350.
PR	16-MAR-2000; 2000US-0189874.
PR	17-MAR-2000; 2000US-0190076.
PR	18-APR-2000; 2000US-0198123.
PR	19-MAY-2000; 2000US-0205315.
PR	07-JUN-2000; 2000US-0209467.
PR	28-JUN-2000; 2000US-0214886.
PR	30-JUN-2000; 2000US-0215135.
PR	07-JUL-2000; 2000US-0216647.
PR	07-JUL-2000; 2000US-0216680.
PR	11-JUL-2000; 2000US-0217487.
PR	11-JUL-2000; 2000US-0217496.
PR	14-JUL-2000; 2000US-0218930.
PR	26-JUL-2000; 2000US-0220963.
PR	26-JUL-2000; 2000US-0220964.
PR	14-AUG-2000; 2000US-0224518.
PR	14-AUG-2000; 2000US-0224519.
PR	14-AUG-2000; 2000US-0225213.
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PR	14-AUG-2000; 2000US-0225266.
PR	14-AUG-2000; 2000US-0225267.
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PR	14-AUG-2000; 2000US-0225270.
PR	14-AUG-2000; 2000US-0225447.
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PR	22-AUG-2000; 2000US-0227182.
PR	23-AUG-2000; 2000US-0227009.
PR	30-AUG-2000; 2000US-0228924.
PR	01-SEP-2000; 2000US-0229287.
PR	01-SEP-2000; 2000US-0229343.
PR	01-SEP-2000; 2000US-0229344.
PR	01-SEP-2000; 2000US-0229345.
PR	05-SEP-2000; 2000US-0229509.
PR	05-SEP-2000; 2000US-0229513.
PR	06-SEP-2000; 2000US-0230437.
PR	06-SEP-2000; 2000US-0230438.
PR	08-SEP-2000; 2000US-0231342.
PR	08-SEP-2000; 2000US-0231343.
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PR	08-SEP-2000; 2000US-0231345.
PR	08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233066.
 PR 14-SEP-2000; 2000US-0233067.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234224.
 PR 25-SEP-2000; 2000US-0234997.
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 PR 02-OCT-2000; 2000US-0236370.
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 PR 02-OCT-2000; 2000US-0237038.
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 PR 20-OCT-2000; 2000US-0241221.
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 PR 08-NOV-2000; 2000US-0246526.
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 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0249207.
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 PR 17-NOV-2000; 2000US-0249216.
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 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.

PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI: 2001-476224/51.
 DR
 XX
 XX
 PT Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the respiratory system including respiratory
 PT cancers and also for testing and detection e.g. diagnosis -
 XX
 XX
 PS Disclosure; SED ID No 1054; 546pp; English.
 XX
 CC The present invention relates to the isolation of novel human
 CC respiratory antigens (AAU17685-AAU17975), and cDNA and genomic
 CC sequences encoding for these polypeptides. The sequences of the
 CC invention are useful for preventing, treating and/or prognosing
 CC disorders related to the respiratory system including throat
 CC disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis),
 CC lung disorders e.g. pneumonia, allergic disorders e.g. asthma,
 CC pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of
 CC the respiratory tissues e.g. lung cancer. The polynucleotide sequences
 CC of the invention are useful in gene therapy and antisense therapy.
 CC AA528161-AA528764 represent genomic sequences encoding for novel
 CC human respiratory antigens.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 14654 BP; 2492 A; 4400 C; 4798 G; 2964 T; 0 other;
 Query Match 80.0%; Score 16.8; DB 22; Length 14654;
 Best Local Similarity 90.0%; Pred. No. 4.1e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 gctggcggaagctggggcc 20
 Db 2043 gctggcggaagctggggcc 2062
 RESULT 14
 AA069840/C
 ID AA069840 standard: DNA; 50 BP.
 XX
 AC AA069840;
 XX
 DT 06-MAR-1995 (first entry)
 XX
 DE Simian virus 40 T/t late (start site 31), target region.
 XX
 KW DNA protein-binding assay; test sequence; screening sequence;
 KW promoter; target; TATA box; Herpes Simplex Virus; HSV;
 KW origin of replication; UL9; transcription factor; TFIID; ds.
 XX
 OS Synthetic.
 XX
 PN W09414980-A.
 XX

```

PD 07-JUL-1994.
XX
XX 20-DEC-1993: 93MO-US12388.
PF
XX 23-DEC-1992: 92US-0996783.
PR 17-SEP-1993: 93US-0123936.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
XX WPI; 1994-234711/28.
DR
XX
XX Sequence-directed DNA-binding molecules - useful in
XX pharmaceuticals and as molecular reagents
XX
XX Claim 28; Page 507; 587pp; English.
XX
XX A DNA protein-binding assay is provided, useful for screening
XX libraries of synthetic or biological cpds. for their ability
XX to bind DNA test sequences. The assay is versatile in that any
XX number of test sequences can be tested by placing the test sequence
XX adjacent to a defined protein-binding screening sequence. Binding
XX of mols. to these test sequences changes the binding characteristics
XX of the protein mol. to its cognate binding sequence. When such a mol.
XX binds the test sequence, the equilibrium of the DNA:protein complexes
XX is disturbed, generating changes in the concentration of free DNA probe.
XX One application of this method is to eucaryotic general transcription
XX factors (e.g. TFIID), where the target region is typically selected
XX from DNA sequences adjacent to the binding site for the eucaryotic
XX transcription factor. Numerous exemplary test sequences are given:
XX the sequences in AA069251-731 and AA069850 correspond to promoter
XX targets (typically, TATA box-contd. sites) for human genes and the
XX sequences in AA065733-849 correspond to promoter targets for viral genes.
XX The test sequences may also be randomly generated. DNA:protein
XX interaction may be used for screening purposes, e.g. the Herpes Simplex
XX virus (HSV) origin of replication and UVS (see AA069851-52, AA069865 and
XX AA069891).
XX
XX Sequence 50 BP; 6 A; 26 C; 8 G; 10 T; 0 other;
SQ

```

```

Query Match 78.1%; Score 16.4; DB 15; Length 50;
Best Local Similarity 94.4%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 ctgggcggaagttggggc 19
    |||||
DB 20 CTGGCGCGAGCTTAGGGC 3

```

```

RESULT 15
AAT64302/c
ID AAT64302 standard; DNA; 50 BP.
XX
XX AAT64302;
AC
XX
XX 17-MAR-1997 (first entry)
DT
XX
XX SV40 T/c late (start site 31) TFIID binding site.
DE
XX
XX Duplex DNA; target region; binding characteristic; DNA binding protein;
XX TFIID; transcription factor; binding site; inhibition; enhance;
KW cancer; inherited genetic disorder; ds.
XX
XX Rhesus macaque polyoma virus.
OS
XX
XX US5578444-A.
PN
XX
XX 26-NOV-1996.
PD
XX
XX 27-JUN-1991; 91US-0723618.
PF
XX

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PR 20-DEC-1993: 93US-0171389.
PR 27-JUN-1991: 91US-0723618.
PR 23-DEC-1992: 92US-0996783.
PR 17-SEP-1993: 93US-0123936.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
XX WPI; 1997-020402/02.
DR
XX
XX Altering binding characteristics of DNA binding proteins to duplex
XX DNA - by attaching specific small cpd. to target region close to the
XX protein's binding site, useful in treatment of viral disease, cancer
XX etc
XX
XX Claim 6; Column 401; 264pp; English.
XX
XX The sequences given in AAT63713-4312 represent duplex DNA's which act
XX as target regions in the method of the invention. The method for
XX altering the binding characteristics of a DNA-binding protein to duplex
XX DNA comprises contacting the duplex DNA with a small molecule which
XX binds sequence-specifically to a target region, where, when the small
XX molecule is bound to the target region, it is adjacent to, but not
XX overlapping by more than 4 bp, a binding site for a DNA-binding protein.
XX The small molecule is added at a concentration effective to alter the
XX binding of the DNA binding protein, pret. TFIID, to its binding site on
XX the duplex DNA. The binding of the small molecule may inhibit or
XX enhance the binding of the DNA-binding protein to its binding site. The
XX compounds isolated using this method are potentially useful as
XX therapeutic agents for treatment of any disease which involves a
XX specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
XX The method is suitable for screening large biological or chemical
XX libraries and allows determination of sequence-specific and relative
XX affinities of known DNA-binding agents for different DNA sequences.
XX The design of these duplex DNA's allows a single DNA:protein interaction
XX to be used for screening sequence-specific, or preferential, DNA binding
XX proteins that recognise almost any possible sequence (see also AAT49539-
XX 74).
XX
XX Sequence 50 BP; 6 A; 26 C; 8 G; 10 T; 0 other;
SQ

```

```

Query Match 78.1%; Score 16.4; DB 16; Length 50;
Best Local Similarity 94.4%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 ctgggcggaagttggggc 19
    |||||
DB 20 CTGGCGCGAGCTTAGGGC 3

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Job time: 7049 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:04:32 ; Search time 1959.41 Seconds
(without alignments)
224.280 Million cell updates/sec

Title: US-09-913-325-12

Perfect score: 21
Sequence: 1 gctggcgagcttggggacct 21

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba:*
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- 3: gb_in:*
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- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_cm:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pal:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
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C	1	21	100.0	975	6	AX014321	AX014321 Sequence
C	2	21	100.0	1416	6	HUMSGLY	M74816 Human sulf
C	3	21	100.0	1512	6	AX302541	AX302541 Sequence
C	4	21	100.0	1512	9	HUMAP01	J02908 Human apol1
C	5	21	100.0	1648	9	HUMTRPM2A	M64722 Human TRPM
C	6	21	100.0	1658	9	BC019588	BC019588 Homo sapi
C	7	21	100.0	1676	6	HSCSP40	X14723 Human SP-40
C	8	21	100.0	1678	6	AX202086	AX202086 Sequence
C	9	21	100.0	1684	6	BC010514	BC010514 Homo sapi
C	10	21	100.0	3196	6	AX330207	AX330207 Sequence
C	11	21	100.0	3196	6	AX337122	AX337122 Sequence
C	12	21	100.0	3196	6	HUMTRPM2A4	M63379 Human TRPM
C	13	21	100.0	8133	9	HUMSEP40A	L00974 Homo sapien
C	14	21	100.0	187453	2	AC025192	AC025192 Homo sapi
C	15	21	100.0	234431	9	AF311103	AF311103 Homo sapi
C	16	18.4	87.6	57722	2	HSCB33B10	Z82175 Homo sapien
C	17	18.4	87.6	76295	2	AC023542	AC023542 Homo sapi
C	18	18.4	87.6	86501	9	AC079171	AC079171 Homo sapi
C	19	18.4	87.6	106008	9	HS506	AL020993 Human DNA
C	20	17.8	84.8	398	12	SYNSV4PYRO	K01476 SV40/polyom
C	21	17.8	84.8	2132	9	HSAB01802	AJ011802 Homo sapi
C	22	17.8	84.8	73396	9	AC008848	AC008848 Homo sapi
C	23	17.8	84.8	114653	2	AC092411	AC092411 Felis cat
C	24	17.8	84.8	143804	2	AC012617	AC012617 Homo sapi
C	25	17.8	84.8	157758	9	AC098824	AC098824 Homo sapi
C	26	17.8	84.8	169638	9	AC009433	AC009433 Homo sapi
C	27	17.8	84.8	179000	2	AC011847	AC011847 Homo sapi
C	28	17.8	84.8	185854	2	AC027736	AC027736 Homo sapi
C	29	17.8	84.8	187640	2	AC095241	AC095241 Rattus no
C	30	17.4	82.9	119452	2	AC090647	AC090647 Mus muscu
C	31	17.4	82.9	119452	2	AC105186	AC105186 Homo sapi
C	32	17.4	82.9	140453	2	AC095285	AC095285 Rattus no
C	33	17.4	82.9	183584	2	AC095195	AC095195 Rattus no
C	34	17.4	82.9	216425	2	AC084825	AC084825 Mus muscu
C	35	17.4	82.9	220376	2	AC025579	AC025579 Mus muscu
C	36	17.4	82.9	241714	2	AC083834	AC083834 Mus muscu
C	37	17	81.0	9738	14	AF164485	AF164485 HIV-1 iso
C	38	16.8	80.0	724	9	HSAB30907	AJ330907 Homo sapi
C	39	16.8	80.0	1111	4	P1GALIP1	D10616 Pig gene fo
C	40	16.8	80.0	1242	4	AF177912	AF177912 Ovis arie
C	41	16.8	80.0	1639	4	BTU08213	U08213 Bos taurus
C	42	16.8	80.0	2170	9	AB03799501	AB037998 Homo sapi
C	43	16.8	80.0	2535	6	AX179295	AX179295 Sequence
C	44	16.8	80.0	2962	6	A98491	A98491 Sequence 1
C	45	16.8	80.0	2962	10	RNC6519	AJ006519 Rattus no

ALIGNMENTS

RESULT	1	AX014321	975 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AX014321/C	Sequence	29 from Patent WO954353.			
DEFINITION	AX014321					
ACCESSION	AX014321					
VERSION	AX014321.1	GI:10040675				
KEYWORDS						
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS		Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarsky,C.				
TITLE		Human nucleic acid sequences of normal uterus tissue				
JOURNAL		Patent: WO 954353-A 29 28-OCT-1999.				
FEATURES		SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)				
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		/db_xref="taxon:9606"				

BASE COUNT 221 a 320 c 248 g 186 t
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Query Match 100.0%; Score 21; DB 6; Length 975;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcggaagtggggcct 21
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Db 903 GCTGGCGGAGTTGGGGCCT 883

RESULT 2
HUMSGLY/c 1416 bp mRNA linear PRI 09-JAN-1995
LOCUS Human sulfated glycoprotein-2 mRNA, 3' end.
DEFINITION M74816
ACCESSION M74816 GI:338056
VERSION
KEYWORDS secreted protein; sulfated glycoprotein-2.
SOURCE Homo sapiens male 63 yr. old adult brain tumor CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1416)
AUTHORS Danik, M., Chabot, J.G., Mercier, C., Benabid, A.L., Chauvin, C.,
Quirion, R. and Suh, M.
TITLE Human gliomas and epileptic foci express high levels of a mRNA
marker of cell death
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8577-8581 (1991)
MEDLINE 92020896
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/db_xref="taxon:9606"
/map="8"
/sex="male"
/cell_type="astrocytoma (gr. III)"
/tissue_type="brain tumor"
/dev_stage="63 yr. old adult"
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/gene="CLT"
<1..1172
/gene="CLT"
/codon_start=3
/product="sulfated glycoprotein-2"
/protein_id="AA60321.1"
/db_xref="GI:338057"
/db_xref="GDB:G00-125-226"
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TMAALMECKPCLKOTCKMFKYARVCNRSGLVGRQLEEFILNOSPPFYVWNGRIDSL
LENDROQTHMLDVQDHSRASSIIDLFDQRETPRQDTYHYLPDLRHPHFEE
PKSRIVRLMPFSYEPLINFAHQDQPELEMIHEQQAQDIHFSPAEQHPPTFIEEG
DDDRVCREIRINSTGCLRMKDCQCREILSVDCSTNNPSQAKLRLEIDELSDVNER
LTRKYNELKSYQMKMLNTSSILEQLEQFNWYSLNLTQGEQVYLRTVTVASHTS
DSDPVSGTEVYTLFSDPTITVTPVEVSRKPKFMETVAERKALQDYRKHKREE"

BASE COUNT 344 a 440 c 365 g 267 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1416;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcggaagtggggcct 21
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Db 1309 GCTGGCGGAGTTGGGGCCT 1289

RESULT 3
AX302541/c 1512 bp DNA linear PAT 30-NOV-2001
LOCUS

DEFINITION Sequence 59 from Patent WO0175177.
ACCESSION AX302541
VERSION AX302541.1 GI:17383080
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Morin, P.J., Sherman-Bauslt, C.A., Pizer, E.S. and Hough, C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patient: WO 0175177-A 59 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
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location/Qualifiers
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BASE COUNT 378 a 461 c 387 g 286 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggcggaagtggggcct 21
|||||
Db 1405 GCTGGCGGAGTTGGGGCCT 1385

RESULT 4
HUMAPOL/c 1512 bp mRNA linear PRI 31-OCT-1994
LOCUS Human apolipoprotein J mRNA, complete cds.
DEFINITION J02908
ACCESSION J02908 GI:178854
VERSION
KEYWORDS apolipoprotein J; high density lipoprotein.
SOURCE Human fetal liver, CDNA to mRNA, clone lambda[d1-3].
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1512)
AUTHORS de Silva, H.V., Harmony, J.A., Stuart, W.D., Gil, C.M. and Robbins, J.
TITLE Apolipoprotein J: structure and tissue distribution
JOURNAL Biochemistry 29 (22), 5380-5389 (1990)
MEDLINE 90344779
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by J. Robbins, 21-MAR-1990.
FEATURES
source 1..1512
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="unassigned"
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/product="apolipoprotein J mRNA"
1..1512
/gene="APOJ"
18..1268
/gene="APOJ"
/note="apolipoprotein J precursor"
/codon_start=1
/protein_id="AA51765.1"
/db_xref="GI:178855"
/db_xref="GDB:13053"
/translation="MSNGSKYVKNKEITONAVNGVQIKTLIEKTNEERKTLISNLEA
KKKEDALNETRESEPKLKEIPGVONETMAALMECKPCLKOTCKMFKYARVCNRSGL
VGRQLEEFILNOSPPFYVWNGRIDSLLENDROQTHMLDVQDHSRASSIIDLFDQ
RETPRQDTYHYLPDLRHPHFEEPKSRIVRLMPFSYEPLINFAHQDQPELEMIHEQQAQ
DIHFSPAEQHPPTFIEEGDDDRVCREIRINSTGCLRMKDCQCREILSVDCSTNNPSQAK
LRLEIDELSDVNERLTRKYNELKSYQMKMLNTSSILEQLEQFNWYSLNLTQGEQVYLRT
VTVASHTSDSDPVSGTEVYTLFSDPTITVTPVEVSRKPKFMETVAERKALQDYRKHKREE"


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mat_peptide      18..599
                  /gene="APOU"
                  /product="apolipoprotein J alpha-subunit"
mat_peptide      600..1265
                  /gene="APOU"
                  /product="apolipoprotein J beta-subunit"
BASE COUNT      378 a      461 c      387 g      286 t
ORIGIN
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Query Match	100.0%	Score 21;	DB 9;	Length 1512;
Best Local Similarity	100.0%	Pred. No. 24;		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Oy	1	gctggcggaagttcggggccct	21
Db	1405	gcTGGGCGAGTTGGGGGCT	1385

RESULT	5		
HUMTRPM2A/C			
LOCUS	HUMTRPM2A	1648 bp	
DEFINITION	Human TRPM-2 mRNA, complete cds.	mRNA	
ACCESSION	M64722		linear
VERSION	M64722.1		
KEYWORDS	TRPM-2 protein.		
SOURCE	Human cDNA to mRNA.		
ORGANISM	Homo sapiens		

Query Match	100.0%;	Score 21;	DB 9;	Length 1648;
Best Local Similarity	100.0%;	Pred. No. 24;		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0
				Gaps 0

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Qy      1  gctggcggaattggggcct  21
          |||||
Db      1541  GCTGGCGGAGTTGGGGCCT  1521
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RESULT	6			
BC019588/c				
LOCUS	BC019588	1658 bp	mRNA	linear
			PRI	22-JAN-2002

LOCUS	BC019588	1658 bp	mRNA	linear	SP1 22-JAN-2002
DEFINITION	Homo sapiens, clusterin (complement lytic inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J), clone MGC:24903 IMAGE:491544, mRNA, complete cds.				
ACCESSION	BC019588				
VERSION	BC019588.1	GI:18043614			
KEYWORDS	MGC.				
SOURCE	human.				

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

REFERENCE 1 (bases 1 to 1658)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRKA Plate: 29 Row: m Column: 21
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502904.
 Location/Qualifiers
 1. .1658

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctggcgagtggtgggacct 21
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Db 1535 GCTGGCGGAGTGGGGCCT 1515

RESULT 7

HSCSP40 1676 bp mRNA linear PRI 22-MAR-1995
LOCUS Human SP-40, 40 mRNA for complement-associated protein SP-40, 40
DEFINITION alpha-1 and beta-1 chain.

ACCESSION X14723.1 GI:30250
VERSION X14723.1
KEYWORDS complement-associated protein; serum protein; SP-40,40 gene.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 1676)
JOURNAL Direct Submission
Submitted (17-MAR-1989) Kirsbaum L., The University of Melbourne,
The Precinctical Centre, School of Veterinary Science, Parkville
Victoria 3052, Australia

REFERENCE

AUTHORS Kirsbaum L., Sharpe, J.A., Murphy, B., d'Apice, A.J., Classon, B.,
Hudson, P. and Walker, I.D.
TITLE Molecular cloning and characterization of the novel, human
complement cloning and characterization of the novel, human
complement and reproductive systems

JOURNAL

EMBO J. 8 (3), 711-718 (1989)
89251601

COMMENT

The sequence overlaps with that reported by Murphy et. al. in J.
Clin. Invest. 81:1858-1864(1988).

FEATURES

source location/Qualifiers
1..1676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LK (107)"
/issue_type="liver"
/clone.lib="lambda gtl1"
48..113
48..1397
/note="SP-40,40 prepropeptide (AA -22 to 427)"
/codon_start=1
/protein_id="CAA32847.1"
/db_xref="GI:30251"
/db_xref="SWISS-PROT:P10909"
/translation="MMKTLFLFGLLITWSSGOVIGDQTVSDNLEQMSNGSKYVN
ETONAVGVAKITLIEKTEERKTLSTLEAKKKKEDLNTERSEYFKALPGVC
NETMMALECKPCDLKQCKYARVCRSGSLVGRLEFLNQSSPEYKWMNGDRD
SLENDROQTHMLDMQDHFSSASIIDELFQRFREPODYHYLPFLPRRHF
EFPKSRIVRSIMPEYPLNFHMFQPLFEMIEAQAADIHFHSPAFQHPTEFR
EGDDRTVCREIRHNSGCLRMKDCDCKREILISVDCSTNNPOAKLRRLDSLOVA
ERLTKRNELKSTQKMKMLTSSLEBLSNQFPMVSLATLQGEQOXYLRVTVASH
TSDSDVPSGVTEVVKLFDSDPITVIVPEVSRKNPFEMETVAEKALQETRKHREP"
114..>114
/note="beta-chain"
114..1394
/note="SP-40,40 prepeptide (AA 1-427)"
729..1394
/product="mature alpha-chain (AA 205-427)"
1622..1627
/note="pot. polyA signal"

BASE COUNT

436 a 488 c 437 g 315 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1676;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctggcgagtggtgggacct 21
|||||
Db 1536 GCTGGCGGAGTGGGGCCT 1516

RESULT 8

AX202086 1678 bp DNA linear PAT 30-AUG-2001
LOCUS Sequence 16 from Patent WO0153531.
DEFINITION AX202086
ACCESSION AX202086
VERSION AX202086.1 GI:15391872
KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Phippard, D., Vasanthakumari, G., Dotson, S. and Ma, X.J.
TITLE Osteoarthritis tissue derived nucleic acids, polypeptides, vectors,
and cells
Patent: WO 0153531-A 16 26-JUL-2001;
Pharmacia Corporation (US)

JOURNAL

FEATURES

source

1..1678
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 424 a 491 c 450 g 313 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 1678;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctggcgagtggtgggacct 21
|||||
Db 1558 GCTGGCGGAGTGGGGCCT 1538

RESULT 9

BC010514 1684 bp mRNA linear PRI 12-JUL-2001
LOCUS Homo sapiens, clusterin (complement lysis inhibitor, SP-40,40,
DEFINITION sulfated glycoprotein 2, testosterone-repressed prostate message 2,
apolipoprotein J), clone MGC:18080 IMAGE:4150452, mRNA, complete
cds.
BC010514
BC010514.1 GI:14714740
/protein_id="MGC:18080"

ACCESSION BC010514
VERSION BC010514.1
KEYWORDS human.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalobebcm.tmc.edu
Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRK Plate: 19 Row: 0 Column: 12.

FEATURES

Source

Location/Qualifiers

1. 1684

/organism="Homo sapiens"

/db_xref="taxon:9606"

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/issue_type="Brain, glioblastoma with EGFR amplification"

/clone_1b="NCI-CGAP_Brn64"

/lab_host="DH10B"

/note="Vector: PCMV-SPORT6"

69. 1418

/product="clusterin (complement lysis inhibitor, SP-40/40, sulfated glycoprotein 2, testosterone-repressed prostate

message 2, apolipoprotein j)"

/protein_id="AAH10514.1"

/db_xref="GI:14714741"

/translation="MMKTLILFVGLITWESGOVIGDOTVSDNELQMSNGSKYVNC EIONAVNGVQITLIEKTEKREKTLISNLEBKKEKELNLTRESEKLELDEVC

NETMALMECKPCLKOTCKEYFARVCSGSLVGLLEPLNOSPFYFWMNGDID

SLENDROQTQHLMDVQDHFSSASSIIDELEFDRFTRPDYTHYPLSPHRRHF

FPEKSRVRSILMPSPYEPLEPHAMEQPLEMEHAQAMDIHFHSPAQHPTEIR

EGDDRTVCREIRHNSGCLRMKODCKGEITLSTVCSNNPSOAKLRELESLQVA

ERLTRYNNELKSYOMKMLNTSLLEINQOEFWMLANLQGEQVYLYRTYVASH

TSDSDVPSGTEVYVLFDSDPITVTPVPEVSKNPKFMEYAEKALQETRRKREE"

BASE COUNT

433 a 433 c 448 g 310 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1684;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctggcgaggtggggcct 21

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Db 1555 GCTGGCGGAGTTGGGGCCT 1535

RESULT 10

AX330207/c

LOCUS AX330207 3196 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 716 from Patent WO0194629.

AX330207

VERSION AX330207.1 GI:18103185

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (sites)
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D.R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature

gene sets
Patent: WO 0194629-A 716 13-DEC-2001;

JOURNAL

Pharmaceuticals (US)

FEATURES

Source

1. 3196

/organism="Homo sapiens"

/db_xref="taxon:9606"

833 a 762 c 789 g 812 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 3196;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctggcgaggtggggcct 21

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Db 2891 GCTGGCGGAGTTGGGGCCT 2871

RESULT 11

AX337122/c

LOCUS AX337122 3196 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 7631 from Patent WO0194629.

AX337122

VERSION AX337122.1 GI:18127841

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (sites)
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D.R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature

gene sets
Patent: WO 0194629-A 7631 13-DEC-2001;

JOURNAL

Pharmaceuticals (US)

FEATURES

Source

1. 3196

/organism="Homo sapiens"

/db_xref="taxon:9606"

833 a 762 c 789 g 812 t

BASE COUNT

Query Match 100.0%; Score 21; DB 6; Length 3196;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctggcgaggtggggcct 21

|||||

Db 2891 GCTGGCGGAGTTGGGGCCT 2871

RESULT 12

HUMTRPM24/c

LOCUS HUMTRPM24 3196 bp DNA linear PRI 23-AUG-1996

DEFINITION Human TRPM-2 protein gene, exons 7, 8, 9 and complete cds.

AX337122

VERSION M63379.1 GI:292841

KEYWORDS

SEGMENT

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (sites)
Wong, P., Pineault, J., Lakin, J., Taillefer, D., Leger, J., Wang, C.

and Tenniswood, M.

Genomic organization and expression of the rat TRPM-2 (clusterin)

gene, a gene implicated in apoptosis

J. Biol. Chem. 268 (7), 5021-5031 (1993)

JOURNAL

Medicine 93186813

2 (bases 1 to 3196)

Wong, P., Taillefer, D., Lakin, J., Pineault, J., Chader, G. and

Tenniswood, M.

Molecular characterization of human TRPM-2/clusterin, a gene

associated with sperm maturation, apoptosis and neurodegeneration

Eur. J. Biochem. 221 (3), 917-925 (1994)

FEATURES

Source

1. 3196

/organism="Homo sapiens"
/db_xref="taxon:9606"
join(M63376.1:1422..1469,M63376.1:5509..5634,
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M63378.1:1247..1351,995..1224,2362..2537,2745..2998)
/gene="TRPM-2"
join(M63376.1:1422..7610,M63377.1:1..940,M63378.1:1..1634,
1..3166)
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join(M63376.1:5538..5634,M63376.1:7021..7169,
M63377.1:155..325,M63378.1:308..719,M63378.1:1247..1351,
995..1224,2362..2537,2745..2754)
/gene="TRPM-2"
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/protein_id="AAB06507.1"
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ETQNAVGVKQIKTLIEKTNDEKRTLLSLEBAKKKEDALNETRESEYKLELPGVC
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SLENDROQTHMDVMQDHFSSASSIIDELFODREFREPQDYHYLPESLPHRRHF
FFPKSRIVRSILMPSPYEPFLNFMQPLFMHIAEQAMDIFHSPAFQHPTEFR
EGDDRTVCREIRHNSGCLRMKDCCKREILISVDCSTNNSQAKRLRELDLSLOVA
ERLTKRYNELLSYQMKMLNFSLEQLEQDFMWSRLANTQGEDQYLRVTVASH
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2362..2537
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2745..2998
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3085..3090
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3146..3151
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3161..3166
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BASE COUNT 833 a 762 c 789 g 812 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctggcgaggttggggcct 21
|||||
Db 2891 GCTGGCGGAGTTGGGGCCT 2871
RESULT 13
LOCUS HUMSP4040A 8133 bp DNA linear PRI 13-JAN-1995
DEFINITION Homo sapiens SP40.40 gene, exons 5-9.
ACCESSION L00974
VERSION L00974.1 GI:338304
KEYWORDS
SOURCE Homo sapiens Foetal Liver DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 8133)
AUTHORS Giew.M.D., Kirsbaum.L., Bozas.S.E. and Walker.I.D.
TITLE Partial nucleotide sequence of the human SP40.40 gene
JOURNAL Unpublished (1993)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="Foetal Liver"
520..7869
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/partial
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/product="SP40.40"
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/db_xref="GI:338305"
/translation="LEEFNQSPPFYFMWNGDRIDSLLENDROQTHMDVMQDHFSSRA
SSIDLEFDREFTREPQDYHYLPESLPHRRPFFPKSRIVRSILMPSPYEPFLNFM
AMQPLELMEHIAEQAMDIFHSPAFQHPTEFRFGDDRTVCREIRHNSGCLRMK
DCCDKREILISVDCSTNNSQAKRLRELDLSLOVAERLTKRYNELLSYQMKMLNFS
LEQLEQDFMWSRLANTQGEDQYLRVTVASHTSQSDVPSGVTEVVKLFDSDP
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7605..7869
/gene="SP40.40"
/number=9
7838..7843
/gene="SP40.40"
8008..8013
POLYA_SIGNAL
8023..8028
BASE COUNT 1982 a 2024 c 2002 g 2125 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 8133;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctggcgaggttggggcct 21
|||||
Db 7752 GCTGGCGGAGTTGGGGCCT 7732
RESULT 14
LOCUS AC025192 187453 bp DNA linear HTG 13-MAY-2001
DEFINITION Homo sapiens chromosome 8 clone RP11-509E2 map 8, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
ACCESSION AC025192
VERSION AC025192.3 GI:12313839
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 187453)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-509E2
2 (bases 1 to 187453)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Batta,N., Bastien,Y., Bede,F.,
Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G.,
Campioano,A., Castle,A., Choedel,Y., Colangelo,M., Collins,S.,
Collimore,A., Cooke,P., Deatellano,K., Dewar,K., Diaz,J.S.,
Dodg,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heathford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczy,J.,

Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R.,
 Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Ollivat, T. M., Oliver, J., Peterson, K., Pierre, N.,
 Pisanil, C., Pollard, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testa, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
 JOURNAL
 COMMENT
 Direct Submission
 Submitted (07-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jan 19, 2001 this sequence version replaced gi:18901239.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

Project Information
 Center project name: L5592
 Center clone name: 509_E_2

Summary Statistics
 Sequencing vector: M13; M77815: 48% of reads
 Sequencing vector: Plasmid; n/a: 52% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 185120 bases at least Q40
 Consensus quality: 185074 bases at least Q30
 Consensus quality: 186533 bases at least Q20
 Insert size: 175000; agarose-ftp
 Insert size: 186853; sum-of-contigs
 Quality coverage: 8.9 in Q20 bases; agarose-ftp
 Quality coverage: 8.3 in Q20 ba.

NOTE: This is a 'working draft' sequence. It currently
 consists of 7 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 17773: contig of 17773 bp in length
 * 17774 17873: gap of 100 bp
 * 17874 20278: contig of 2405 bp in length
 * 20279 20378: gap of 100 bp
 * 20379 35742: contig of 15364 bp in length
 * 35743 35842: gap of 100 bp
 * 35843 65413: contig of 29571 bp in length
 * 65414 65513: gap of 100 bp
 * 65514 112793: contig of 47280 bp in length
 * 112794 112893: gap of 100 bp
 * 112894 150031: contig of 37138 bp in length
 * 150032 150131: gap of 100 bp
 * 150132 187453: contig of 37322 bp in length.

FEATURES

source

1. 187453
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8"

misc_feature
 1. 17773
 /clone_lib="RP11 Human Male BAC"
 /note="assembly_fragment"

misc_feature
 17874..20278
 /note="assembly_fragment"

misc_feature 20379..35742
 /note="assembly_fragment"
 misc_feature 35843..65413
 /note="assembly_fragment"
 misc_feature 65514..112793
 /note="assembly_fragment"
 misc_feature 112894..150031
 /note="assembly_fragment"
 misc_feature 150132..187453
 /note="assembly_fragment"
 clone_end:17
 vector_side:right

Query Match 100.0%; Score 21; DB 2; Length 187453;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctgggcgagctgggagcct 21
 |||||
 Db 137322 GCTGGGCGAGCTGGGCGCCT 137302

RESULT 15
 AF311103/c 234431 bp DNA linear PRI 06-FEB-2002
 LOCUS Homo sapiens chromosome 8 clone SCB-212e3 map 8p12, complete
 DEFINITION
 ACCESSION AF311103 GI:18542957
 VERSION AF311103.3
 KEYWORDS HTG: HTGS_FULTOP; HTGS_ACTIVIERIN.
 SOURCE human.
 ORGANISM human.

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 234431)
 Wen, G., Blechschmidt, K., Baumgart, C., Taudin, S., Baumgart, C. and
 Platzer, M.

TITLE
 JOURNAL Chromosome 8 genomic sequence
 2 (bases 1 to 234431)
 Blechschmidt, K., Jandrig, B., Baumgart, C., Dette, M. D., Jahn, N.,
 Menzel, U., Schillabel, M. B., Wen, G., Taudien, S. and Rosenthal, A.

TITLE
 JOURNAL Direct Submission
 Submitted (04-OCT-2000) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
 3 (bases 1 to 234431)
 Wen, G. and Platzer, M.

REFERENCE
 AUTHORS Direct Submission
 Submitted (06-FEB-2002) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
 On Feb 6, 2002 this sequence version replaced gi:14389409.

COMMENT
 ----- Genome Center
 Center: Institute of Molecular Biotechnology
 Center code: IMB
 Web site: http://genome.imb-jena.de/
 Contact: gscj-submit@genome.imb-jena.de
 ----- Project Information
 Center project name: H319
 Center clone name: SCB-212e3

----- Summary Statistics
 Sequencing vector: M13; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 233404 bases at least Q40
 Consensus quality: 234413 bases at least Q30
 Consensus quality: 234428 bases at least Q20
 Quality coverage: 5.81 x in Q20 bases; sum-of-contigs

----- Sequence Quality Assessment:
 This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

FEATURES
 Source

Location/Qualifiers
 1. .234431
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8p12"
 /clone="SCb-212e3"

BASE COUNT 62993 a 56257 c 55890 g 59291 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 234431;

Best Local Similarity 100.0%; Pred. NO. 14;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctgggcyagttggggcct 21
 |||||
 DB 26443 GCTGGCGGAGTTGGGGCCT 26423

Search completed: May 17, 2002, 16:04:42
 Job time: 16142 sec